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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:55:26 ; Search time 22 Seconds

(without alignments)
1095.879 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391

Sequence: 1 MTELPAPLSTFQNAQMSDN.....ATDYVQPFMDQAFHQFYI 467

Scoring table: BIOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2391	100.0	467	3	US-08-706-344C-30
2	2384	99.7	467	3	US-08-706-344C-32
3	2379	99.5	467	3	US-08-706-344C-32
4	2378	99.5	467	2	US-08-967-101-134
5	2378	99.5	467	2	US-08-967-101-134
6	2378	99.5	467	3	US-08-967-101-134
7	2378	99.5	467	3	US-08-967-101-134
8	2378	99.5	467	3	US-08-967-101-134
9	2378	99.5	467	3	US-08-967-101-134
10	2378	99.5	467	3	US-08-967-101-134
11	2378	99.5	467	3	US-08-967-101-134
12	2378	99.5	467	3	US-08-967-101-134
13	2378	99.5	467	3	US-08-967-101-134
14	2378	99.5	467	3	US-08-967-101-134
15	2378	99.5	467	3	US-08-967-101-134
16	2378	99.5	467	3	US-08-967-101-134
17	2378	99.5	467	3	US-08-967-101-134
18	2378	99.5	467	3	US-08-967-101-134
19	2378	99.5	467	3	US-08-967-101-134
20	2378	99.5	467	3	US-08-967-101-134
21	2378	99.5	467	3	US-08-967-101-134
22	2378	99.5	467	3	US-08-967-101-134
23	2378	99.5	467	3	US-08-967-101-134
24	2378	99.5	467	3	US-08-967-101-134
25	2378	99.5	467	3	US-08-967-101-134
26	2378	99.5	467	3	US-08-967-101-134
27	2378	99.5	467	3	US-08-967-101-134

28	2366	99.0	467	4	US-09-896-621B-5	Sequence 5, Appli
29	2356	98.5	467	4	US-09-896-621B-6	Sequence 6, Appli
30	2348	98.2	463	3	US-08-670-964-4	Sequence 4, Appli
31	2342	98.0	463	3	US-08-888-077A-4	Sequence 4, Appli
32	2333	97.6	463	4	US-08-937-834-6	Sequence 6, Appli
33	2325	97.2	463	2	US-08-670-479-18	Sequence 16, Appli
34	2291	95.8	462	3	US-08-788-231A-15	Sequence 15, Appli
35	2288	95.2	467	3	US-08-888-077A-17	Sequence 17, Appli
36	2228	93.2	467	2	US-08-496-841C-136	Sequence 136, App
37	2178	91.1	467	2	US-08-667-101-4	Sequence 4, Appli
38	2178	91.1	467	2	US-08-592-541-4	Sequence 4, Appli
39	2178	91.1	467	3	US-09-124-698-4	Sequence 4, Appli
40	2178	91.1	467	3	US-09-127-480-4	Sequence 4, Appli
41	2178	91.1	467	3	US-08-496-841C-4	Sequence 4, Appli
42	2178	91.1	467	4	US-09-124-523-4	Sequence 4, Appli
43	2178	91.1	467	4	US-09-636-796A-4	Sequence 4, Appli
44	2178	91.1	467	4	US-08-431-048F-4	Sequence 4, Appli
45	2174.5	90.9	465	3	US-08-788-231A-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-706-344C-30
Sequence 30, Application US/08706344C
Patent No. 6248555
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCOT, WILLIAM
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,344C
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 609.4180001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-344C-30

Query Match 100.0%; Score 2391; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-234;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTELPAPLSTFQNAQMSDNLTNRQENRDRSGHPPLNGRPGQNSR 60
|||||

Db 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLNSGRPOGNSR 60

QY 61 QVVEDEDEDEBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSPYTRKQGLIYTPFTE 120

Db 61 QVVEDEDEDEBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSPYTRKQGLIYTPFTE 120

QY 121 DTEVQGRALHSILNAAIMISIVYMTLLVLYKYRCYKITHAMLISSLLFFPSFI 180

Db 121 DTEVQGRALHSILNAAIMISIVYMTLLVLYKYRCYKITHAMLISSLLFFPSFI 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

Db 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

QY 241 LPBMTAMLIAYISYVDVAVALCKGPRMLVETQENETLFPALISYSTMVWLVNAAE 300

Db 241 LPBMTAMLIAYISYVDVAVALCKGPRMLVETQENETLFPALISYSTMVWLVNAAE 300

QY 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

Db 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

QY 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLVGKASATAGDMMTTIACFVALIGLCL 420

Db 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLVGKASATAGDMMTTIACFVALIGLCL 420

QY 421 TLLLLAIFKKALPALPISITGLVFYFATDYLVPFMDQLAFHQFYI 467

Db 421 TLLLLAIFKKALPALPISITGLVFYFATDYLVPFMDQLAFHQFYI 467

RESULT 2

US-08-706-344C-2

Sequence 2, Application US/08706344C

Patent No. 6248555

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

APPLICANT: MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial

TITLE OF INVENTION: Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,344C

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-706-344C-2

Query Match 99.7%; Score 2384; DB 3; Length 467;

Best Local Similarity 99.8%; Pred. No. 5,5e-234;

Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLNSGRPOGNSR 60

Db 1 MTELPAPLSYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLNSGRPOGNSR 60

QY 61 QVVEDEDEDEBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSPYTRKQGLIYTPFTE 120

Db 61 QVVEDEDEDEBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSPYTRKQGLIYTPFTE 120

QY 121 DTEVQGRALHSILNAAIMISIVYMTLLVLYKYRCYKITHAMLISSLLFFPSFI 180

Db 121 DTEVQGRALHSILNAAIMISIVYMTLLVLYKYRCYKITHAMLISSLLFFPSFI 180

QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

Db 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMKGPRLQQAAYLIMISALMALVFIKY 240

QY 241 LPBMTAMLIAYISYVDVAVALCKGPRMLVETQENETLFPALISYSTMVWLVNAAE 300

Db 241 LPBMTAMLIAYISYVDVAVALCKGPRMLVETQENETLFPALISYSTMVWLVNAAE 300

QY 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

Db 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360

QY 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLVGKASATAGDMMTTIACFVALIGLCL 420

Db 361 VOELSSSILAGDEPERGVKGLGDFIFYSVLVGKASATAGDMMTTIACFVALIGLCL 420

QY 421 TLLLLAIFKKALPALPISITGLVFYFATDYLVPFMDQLAFHQFYI 467

Db 421 TLLLLAIFKKALPALPISITGLVFYFATDYLVPFMDQLAFHQFYI 467

RESULT 3

US-08-706-344C-2

Sequence 32, Application US/08706344C

Patent No. 6248555

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

APPLICANT: MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial

TITLE OF INVENTION: Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,344C

FILING DATE: 30-AUG-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-706-344C-32

Query Match 99.5%; Score 2379; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.8e-233;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
 QY 61 QVVEQDEEDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRDGLITPTPE 120
 DB 61 QVVEQDEEDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRDGLITPTPE 120
 QY 121 DTEVGOALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
 DB 121 DTEVGOALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
 QY 181 YGVEFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKX 240
 DB 181 YGVEFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKX 240
 QY 241 LPEWTAMLIIVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIVYSTWVLVNMAL 300
 DB 241 LPEWTAMLIIVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIVYSTWVLVNMAL 300
 QY 301 GDEPQRRVSKSKNAESTERESQDTVAENDGFSSEMEARQDSHLPHRSTPESRAA 360
 DB 301 GDEPQRRVSKSKNAESTERESQDTVAENDGFSSEMEARQDSHLPHRSTPESRAA 360
 QY 361 VOELSSILAGEDPERGVKLGDFIFYSVLVGRASATASGDMNTTIACFVAIIIGLCL 420
 DB 361 VOELSSILAGEDPERGVKLGDFIFYSVLVGRASATASGDMNTTIACFVAIIIGLCL 420
 QY 421 TLLLAIFKALPALPISITFGIVFYFATDYLVOFMDLAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGIVFYFATDYLVOFMDLAFHQFYI 467

RESULT 4

US-08-967-101-134
 Sequence 134, Application US/08967101
 Patent No. 5840540
 GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PETER H
 APPLICANT: ROMMENS, JOHANNA M
 APPLICANT: FRASER, PAUL E
 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 183
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 STREET: High Street Tower - 125 High Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/967,101
 FILING DATE: 10-NOV-1997

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CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/592,541
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Pichez, Edmund R.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-967-101-134

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPOGNSR 60
 QY 61 QVVEQDEEDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRDGLITPTPE 120
 DB 61 QVVEQDEEDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTRDGLITPTPE 120
 QY 121 DTEVGOALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
 DB 121 DTEVGOALHSILNAAIMISIVVMTLLVLYKRCYKVIHAWLIISLLFFESFI 180
 QY 181 YGVEFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKX 240
 DB 181 YGVEFTYVAVDYITVALLINFGVGMISIHMKGPLRLOQAYLIMSALMAVFIKX 240
 QY 241 LPEWTAMLIIVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIVYSTWVLVNMAL 300
 DB 241 LPEWTAMLIIVSYVDLVAVLCLKGPLMLVETAQERNETLFPALIVYSTWVLVNMAL 300
 QY 301 GDEPQRRVSKSKNAESTERESQDTVAENDGFSSEMEARQDSHLPHRSTPESRAA 360
 DB 301 GDEPQRRVSKSKNAESTERESQDTVAENDGFSSEMEARQDSHLPHRSTPESRAA 360
 QY 361 VOELSSILAGEDPERGVKLGDFIFYSVLVGRASATASGDMNTTIACFVAIIIGLCL 420
 DB 361 VOELSSILAGEDPERGVKLGDFIFYSVLVGRASATASGDMNTTIACFVAIIIGLCL 420
 QY 421 TLLLAIFKALPALPISITFGIVFYFATDYLVOFMDLAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGIVFYFATDYLVOFMDLAFHQFYI 467

RESULT 5

US-08-592-541-134
 Sequence 134, Application US/08592541
 Patent No. 5986054
 GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PETER H
 APPLICANT: ROMMENS, JOHANNA M
 APPLICANT: FRASER, PAUL E
 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 183
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 STREET: High Street Tower - 125 High Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110

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COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/592,541
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Pletcher, Edmund R.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 134:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-592-541-134

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNRERQEHNDRSLSGHEPLNSNGRPOGNSR 60
 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNRERQEHNDRSLSGHEPLNSNGRPOGNSR 60
 61 QVVEQDEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTKDGQILYTPETE 120
 61 QVVEQDEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTKDGQILYTPETE 120
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 361 VOELSSSILAGEDEEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAVAILIGCL 420
 361 VOELSSSILAGEDEEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAVAILIGCL 420
 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOPEMDQLAFHOFYI 467
 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOPEMDQLAFHOFYI 467

RESULT 6
 US-08-923-454A-10
 Sequence 10, Application US/08923454A
 Patent No. 6004724
 GENERAL INFORMATION:
 APPLICANT: Creasy, Caretha
 APPLICANT: Livi, George
 APPLICANT: Kattan, Eric
 APPLICANT: Clinkebeard, Helen
 APPLICANT: Browne, Michael
 APPLICANT: Southern, Christopher
 TITLE OF INVENTION: HUMAN SERINE PROTEASE
 NUMBER OF SEQUENCES: 40

B.1.1.1.1

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923,454A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/025436
 FILING DATE: 06-SEPT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Baumeister, Kirk
 REGISTRATION NUMBER: 33,833
 REFERENCE/DOCKET NUMBER: P50547
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5096
 TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHEICAL: NO
 AMI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 US-08-923-454A-10

Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNRERQEHNDRSLSGHEPLNSNGRPOGNSR 60
 1 MTELPAPLSYFQNAQMSQEDNLSNTVRSQNDNRERQEHNDRSLSGHEPLNSNGRPOGNSR 60
 61 QVVEQDEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTKDGQILYTPETE 120
 61 QVVEQDEEEDBELTLKYGAKHVMLEFVPTLCMVVVAATIKSVFTKDGQILYTPETE 120
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 121 DTEVGGRAHLSINAAIMISIVVMTLLVLYKRCYKVIHMLIISLLFFFSFI 180
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMALVPIKY 240
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 241 LPEWTAMILLAVISYVDLVAVLCRPLRLVETAOENETLFPALISSTWMLVNMAL 300
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLPGRSTPESRAA 360
 361 VOELSSSILAGEDEEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAVAILIGCL 420
 361 VOELSSSILAGEDEEERGVKLGDFIFYSVLVGKASATASGDMNTTIACFAVAILIGCL 420
 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOPEMDQLAFHOFYI 467
 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOPEMDQLAFHOFYI 467

DB 121 DTEVQGRALHSITNAIMISVIVMTILLVLYKRCYKVIHAWLISLLEFFSFI 180
QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLLQOAYILMISALMAVFIKY 240
DB 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLLQOAYILMISALMAVFIKY 240
QY 241 LPFWTAMLLIAVISVYDLVAVLCLKGPLRLVETAOERNETLPPALISSTWMLVNMAL 300
DB 241 LPFWTAMLLIAVISVYDLVAVLCLKGPLRLVETAOERNETLPPALISSTWMLVNMAL 300
QY 301 GDEPAORRVSKNSKXNAESTERESQDTVAENDDGFSEMEAOGRSHLGHRSSTPESRAA 360
DB 301 GDEPAORRVSKNSKXNAESTERESQDTVAENDDGFSEMEAOGRSHLGHRSSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLLAFKKALPALPISITFGVVFYFATDYLVOPMDQLAFHOYI 467
DB 421 TLLLLAFKKALPALPISITFGVVFYFATDYLVOPMDQLAFHOYI 467

RESULT 9

US-09-124-698-134
Sequence 134, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBAUT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-124-698-134

Carlson

Query March 99.5%, Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%, Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTFQNAQMSDNHLSNTVRSQNDNRERQSHNDRSLGHPEPLSNRPOGNSR 60

DB 1 MTELPAPLSTFQNAQMSDNHLSNTVRSQNDNRERQSHNDRSLGHPEPLSNRPOGNSR 60
QY 61 QVSEODEEDELTKYGAHVIMLFVPTLQWVVAVATIKSVSFYTRKDGQIYPTFE 120
DB 61 QVSEODEEDELTKYGAHVIMLFVPTLQWVVAVATIKSVSFYTRKDGQIYPTFE 120
QY 121 DTEVQGRALHSITNAIMISVIVMTILLVLYKRCYKVIHAWLISLLEFFSFI 180
DB 121 DTEVQGRALHSITNAIMISVIVMTILLVLYKRCYKVIHAWLISLLEFFSFI 180
QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLLQOAYILMISALMAVFIKY 240
DB 181 YLGEVFTYVAVDYITVALLINFGVGMISIMWKGPLLQOAYILMISALMAVFIKY 240
QY 241 LPFWTAMLLIAVISVYDLVAVLCLKGPLRLVETAOERNETLPPALISSTWMLVNMAL 300
DB 241 LPFWTAMLLIAVISVYDLVAVLCLKGPLRLVETAOERNETLPPALISSTWMLVNMAL 300
QY 301 GDEPAORRVSKNSKXNAESTERESQDTVAENDDGFSEMEAOGRSHLGHRSSTPESRAA 360
DB 301 GDEPAORRVSKNSKXNAESTERESQDTVAENDDGFSEMEAOGRSHLGHRSSTPESRAA 360
QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVSKASATASGDMNTTIACFVALILGLCL 420
QY 421 TLLLLAFKKALPALPISITFGVVFYFATDYLVOPMDQLAFHOYI 467
DB 421 TLLLLAFKKALPALPISITFGVVFYFATDYLVOPMDQLAFHOYI 467

RESULT 10

US-09-127-480-134
Sequence 134, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBAUT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

Calk
meyer.

MOLECULE TYPE: Protein
US-09-127-480-134

Query Match 99.5%; Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAFLSYFQNAQMSDNHLSNTVRSQNDNREERQENHNDRLSGHPRLSNRPGQNSR 60
DB 1 MTELPAFLSYFQNAQMSDNHLSNTVRSQNDNREERQENHNDRLSGHPRLSNRPGQNSR 60
QY 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVSFYTRKDGQILYTPPTE 120
DB 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVSFYTRKDGQILYTPPTE 120
QY 121 DTEVGGORALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLLPFFSFI 180
DB 121 DTEVGGORALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLLPFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMHKGPLRLQQAVALIMISALMALVFIFY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMHKGPLRLQQAVALIMISALMALVFIFY 240
QY 241 LPEWTAMLLAVISYDVAVALCKGPLRLMVELTAQERNETLFPALITYSTWMLVNMAL 300
DB 241 LPEWTAMLLAVISYDVAVALCKGPLRLMVELTAQERNETLFPALITYSTWMLVNMAL 300
QY 301 GDEPQRRVSKSKNAESTERESODTVAENDDGFSEMEARQDHLGPHRSTPESRAA 360
DB 301 GDEPQRRVSKSKNAESTERESODTVAENDDGFSEMEARQDHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQLAFHQFYI 467

RESULT 11

US-08-496-841C-134
Sequence 134, Application US/08496841C
Patent No. 6210939

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSES: Darby & Darby, PC

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehner, Ph.D.

REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 134:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 134

Query Match 99.5%; Score 2378; DB 3; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAFLSYFQNAQMSDNHLSNTVRSQNDNREERQENHNDRLSGHPRLSNRPGQNSR 60
DB 1 MTELPAFLSYFQNAQMSDNHLSNTVRSQNDNREERQENHNDRLSGHPRLSNRPGQNSR 60
QY 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVSFYTRKDGQILYTPPTE 120
DB 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVAATIKSVSFYTRKDGQILYTPPTE 120
QY 121 DTEVGGORALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLLPFFSFI 180
DB 121 DTEVGGORALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLLPFFSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMHKGPLRLQQAVALIMISALMALVFIFY 240
DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIMHKGPLRLQQAVALIMISALMALVFIFY 240
QY 241 LPEWTAMLLAVISYDVAVALCKGPLRLMVELTAQERNETLFPALITYSTWMLVNMAL 300
DB 241 LPEWTAMLLAVISYDVAVALCKGPLRLMVELTAQERNETLFPALITYSTWMLVNMAL 300
QY 301 GDEPQRRVSKSKNAESTERESODTVAENDDGFSEMEARQDHLGPHRSTPESRAA 360
DB 301 GDEPQRRVSKSKNAESTERESODTVAENDDGFSEMEARQDHLGPHRSTPESRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSVLVGRKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQLAFHQFYI 467
DB 421 TLLLAIFKKALPALPISITFGLVFFATDYLVOQPMQLAFHQFYI 467

RESULT 12

US-08-832-867-3
Sequence 3, Application US/08832867C

Patent No. 6376239

GENERAL INFORMATION:

APPLICANT: BAUMEISTER, Ralf

TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN

C. TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.

FILE REFERENCE: 674503-2004

CURRENT APPLICATION NUMBER: 1997-04-04

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 3

LENGTH: 467

TYPE: PRT

ORGANISM: Caenorhabditis elegans

US-08-832-867-3

Query Match 99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2,2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MTELPAFLSYFQNAQMSDNHLSNTVRSQNDNREERQENHNDRLSGHPRLSNRPGQNSR 60

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Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREROENDRSLGHEPPLSNGRPOGNSR 60
Qy      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120
Db      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120
Qy      121 DTEVGOBALHSILNAINMSIVVMTILLVLYKRCYKVIHAMLIISLLLPFFSFI 180
Db      121 DTEVGOBALHSILNAINMSIVVMTILLVLYKRCYKVIHAMLIISLLLPFFSFI 180
Qy      181 YLGEVFTKYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVYIMTSALMALVFIKY 240
Db      181 YLGEVFTKYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVYIMTSALMALVFIKY 240
Qy      241 LPEWTAMLIASVVDLVAVLCLKGPLRLMVEAQRNETLFPALITYSSTWMLVYMAE 300
Db      241 LPEWTAMLIASVVDLVAVLCLKGPLRLMVEAQRNETLFPALITYSSTWMLVYMAE 300
Qy      301 GDEPAQRVSKNSKNNAESTERESODTVAENDOGFSEWEAQRDHLGPHRSTPESRAA 360
Db      301 GDEPAQRVSKNSKNNAESTERESODTVAENDOGFSEWEAQRDHLGPHRSTPESRAA 360
Qy      361 VOELSSITLAGEPDEERGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
Db      361 VOELSSITLAGEPDEERGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
Qy      421 TLILLAIFKKALPALPISITFGLVFYFATDYLVOFMDQIAFHQFYI 467
Db      421 TLILLAIFKKALPALPISITFGLVFYFATDYLVOFMDQIAFHQFYI 467

RESULT 13
US-09-227-725A-1
; Sequence 1, Application US/09227725A
; Patent No. 6383758
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; FILE REFERENCE: 1034/1F810-US1
; CURRENT APPLICATION NUMBER: US/09/227,725A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-227-725A-1

Query Match      99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREROENDRSLGHEPPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREROENDRSLGHEPPLSNGRPOGNSR 60
Qy      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120
Db      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120
Qy      121 DTEVGOBALHSILNAINMSIVVMTILLVLYKRCYKVIHAMLIISLLLPFFSFI 180
Db      121 DTEVGOBALHSILNAINMSIVVMTILLVLYKRCYKVIHAMLIISLLLPFFSFI 180
Qy      181 YLGEVFTKYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVYIMTSALMALVFIKY 240
Db      181 YLGEVFTKYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVYIMTSALMALVFIKY 240

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Qy      241 LPEWTAMLIASVVDLVAVLCLKGPLRLMVEAQRNETLFPALITYSSTWMLVYMAE 300
Db      241 LPEWTAMLIASVVDLVAVLCLKGPLRLMVEAQRNETLFPALITYSSTWMLVYMAE 300
Qy      301 GDEPAQRVSKNSKNNAESTERESODTVAENDOGFSEWEAQRDHLGPHRSTPESRAA 360
Db      301 GDEPAQRVSKNSKNNAESTERESODTVAENDOGFSEWEAQRDHLGPHRSTPESRAA 360
Qy      361 VOELSSITLAGEPDEERGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
Db      361 VOELSSITLAGEPDEERGVLGLGDFIFYSVLVGKASATASGDMNTTIACFVALILGLCL 420
Qy      421 TLILLAIFKKALPALPISITFGLVFYFATDYLVOFMDQIAFHQFYI 467
Db      421 TLILLAIFKKALPALPISITFGLVFYFATDYLVOFMDQIAFHQFYI 467

RESULT 14
US-09-124-523-134
; Sequence 134, Application US/09124523
; Patent No. 6393960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESSES:
; ADDRESS: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-124-523-134

Query Match      99.5%; Score 2378; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-233;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREROENDRSLGHEPPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNREROENDRSLGHEPPLSNGRPOGNSR 60
Qy      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120
Db      61 QVVEODEBEDEBLTKYGAHVIMLFVPTLCMNVVAVATIKSVFTRKQGLIYTPPTE 120

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QY 121 DTEVGOALHSILNAAMISVIVMTTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGOALHSILNAAMISVIVMTTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFVGVGMTSIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFVGVGMTSIHMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPBWTAMLLIAYISYDVAVALCKGPLRMVETAOERNETLFPALITYSTWVLVMAE 300
 DB 241 LPBWTAMLLIAYISYDVAVALCKGPLRMVETAOERNETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHERSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHERSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKGLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKGLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467

RESULT 15 US-09-375-318-3

Sequence 3, Application US/09375318
 Patent No. 6468791

GENERAL INFORMATION:

APPLICANT: Tenzi, Rudolph E.

Schellenderg, Gerard D.

Masco, Wilma

Levy-Ianad, Ephrat

Bird, Thomas D.

Galas, David J.

TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BEERY LLP

STREET: 701 Fifth Ave, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/375,318

FILING DATE: 16-Aug-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Verma, James M.

REGISTRATION NUMBER: 33,287

REFERENCE/DOCKET NUMBER: 920010.571C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-375-318-3

Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-233;

Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSYFONAOSEBNI:SNVRSQNDREOEHNDRSLGHPERLSGRPOGNSR 60
 DB 1 MTELPAPLSYFONAOSEBNI:SNVRSQNDREOEHNDRSLGHPERLSGRPOGNSR 60
 QY 61 QVEODEEEDDELTLYKGAHVIMLFPVTLQMVVVAITKSVSFYTRDQGLIYTPFE 120
 DB 61 QVEODEEEDDELTLYKGAHVIMLFPVTLQMVVVAITKSVSFYTRDQGLIYTPFE 120
 QY 121 DTEVGOALHSILNAAMISVIVMTTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGOALHSILNAAMISVIVMTTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFVGVGMTSIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFVGVGMTSIHMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPBWTAMLLIAYISYDVAVALCKGPLRMVETAOERNETLFPALITYSTWVLVMAE 300
 DB 241 LPBWTAMLLIAYISYDVAVALCKGPLRMVETAOERNETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHERSTPESRAA 360
 DB 301 GDEPAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDSHLGPHERSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKGLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKGLGDFIFYSVLVGRASATASGDMNTTACFVALIIGLCL 420
 QY 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467
 DB 421 TLLILAIFKKALPALPISITFGLVFYFATDYLVOPFMDOLAFHQFYI 467

Search completed: April 8, 2004, 16:59:19
 Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 16:54:31 ; Search time 21 Seconds

(without alignments)
2139.116 Million cell updates/sec

Title: US-09-785-474a-30

Perfect score: 2391

Sequence: 1 MTELPAPLSTYFQNAQMSDNL.....ATDYLQPMQDLAFHQFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: PIR 789*

1: Dirl:*
2: Dirl:*
3: Dirl:*
4: Dirl:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	99.5	467	2 S58396	presenilin 1, sp1
2	2348	98.2	463	2 S63683	presenilin 1-463
3	2266	94.8	467	2 UC5080	presenilin 1 prote
4	2236	93.5	463	2 UC5081	presenilin 1 prote
5	2228	93.2	467	2 I78388	5182 protein - mou
6	1801	75.3	433	2 UC5390	presenilin-alpha
7	1584	66.2	374	2 S63684	presenilin 1, sp1
8	1462.5	61.2	449	2 UC5391	presenilin-beta
9	1444	60.4	448	2 A56933	presenilin 2 - hum
10	1376.5	57.6	442	2 I39174	seven trans-membra
11	1054.5	44.1	836	2 E89453	protein F35H12.3 l
12	963.5	40.3	461	2 S60253	se1-12 protein - C
13	539.5	22.6	453	2 T00724	presenilin homolog
14	538	22.5	397	2 A84702	probable presenili
15	505	21.1	358	2 T15184	presenilin-beta ho
16	309.5	12.9	465	2 T77885	sperm membrane pro
17	122.5	5.5	455	2 H97237	membrane associate
18	120.5	5.0	2386	2 T39911	rad3 checkpoint pr
19	118.5	5.0	309	2 H90548	hypothetical prote
20	117	4.9	601	2 S12004	tyramine receptor
21	115	4.8	364	2 D95959	conserved hypochet
22	115	4.8	601	2 UH0170	octopamine recepto
23	114.5	4.8	323	2 A88997	tumor surface anti
24	111.5	4.7	339	2 C71132	hypothetical prote
25	110	4.6	318	2 B84291	hypothetical prote
26	110	4.6	707	2 T09340	hypothetical prote
27	109.5	4.6	598	2 T05130	hypothetical prote
28	109	4.6	599	2 T24333	hypothetical prote
29	108.5	4.5	887	2 S73768	MD277 homolog Fl1

ALIGNMENTS

RESULT 1

S58396
presenilin 1, splice form 467 - human

C/Species: Homo sapiens (man)
C/Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999

C/Accession: S58396; S71401; S71402
R/Sherrington, R.; Roqaeve, E.I.; Liang, Y.; Roqaeve, E.A.; Levesque, G.; Ikeda, M.; Ch
ero, I.; Piness, L.; Nee, L.; Chumakov, I.; Pollen, D.; Brookes, A.; Sansau, P.; Pol
E.; Rommens, J.M.; St George-Hyslop, P.H.
Nature 375, 754-760, 1995

A/Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer
A/Reference number: 158095; PMID:95319502; PMID:7596406

A/Accession: S58396
A/Molecule type: mRNA
A/Residues: 1-467 <SHE>

A/Cross-references: EMBL:142110; NID:9904118; PIRN:AB46416.1; PID:9904119
R/Vidal, R.; Ghiso, J.; Wisniewski, T.; Frangione, B.
FEBS Lett. 393, 19-23, 1996

A/Title: Alzheimer's presenilin 1 gene expression in platelets and megakaryocytes. Ider
A/Reference number: S71401; PMID:96397521; PMID:8804415
A/Accession: S71401

A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 24-32;254-256;290-292;316-317;376-379 <VIW>

A/Experimental source: Dani megakaryotic cell line (ATCC CRL-9792) and platelets
C/Genetics:
A/Genes: GDB:PSEN1; AD3; FAD; S182; PS1

A/Cross-references: GDB:135682; OMIM:104311
A/Map position: 14q24.3-14q24.3
C/Suprafamily: presenilin

C/Keywords: alternative splicing; Alzheimer's disease; glycoprotein; transmembrane prot
F/82-100/Domain: transmembrane #status predicted <TM1>
F/133-154/Domain: transmembrane #status predicted <TM2>

F/164-185/Domain: transmembrane #status predicted <TM3>
F/195-213/Domain: transmembrane #status predicted <TM4>
F/221-238/Domain: transmembrane #status predicted <TM5>

F/244-264/Domain: transmembrane #status predicted <TM6>
F/281-301/Domain: transmembrane #status predicted <TM7>
F/406-426/Domain: transmembrane #status predicted <TM8>

F/433-453/Domain: transmembrane #status predicted <TM9>
F/479/405/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 99.5%; Score 2378; DB 2; Length 467;
Best local similarity 99.6%; Pred. No. 1.3e-17;
Matches 465; Conservative 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNLSTVRSQNDNRREQENDRRSLGHPPLNSGRPOGNSR 60
DB 1 MTELPAPLSTYFQNAQMSDNLSTVRSQNDNRREQENDRRSLGHPPLNSGRPOGNSR 60
QY 61 QVVEQDEDEDEDELTLYGAKXIVMLFVPTLCMVVVATIXSVSFYTRKQGLIYPTPE 120

Db 421 TLLLAIFKKALPALPISITFGLVFATDYLVQPFMDQLAFHQFYI 467

RESULT 4

JC5081

presentin 1 protein isoform 463 - lesser mouse lemur
 C/Species: Microcebus murinus (lesser mouse lemur)
 C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
 C/Accession: J05081
 R/Calender, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Pelter, A.; Bone, N.; Bellis, Biochem. Biophys. Res. Commun. 228, 430-439, 1996
 A/Title: Molecular cloning, sequencing, and brain expression of the presentin 1 gene in A. Reference number: J05081; MUID:97079199; PMID:8920831
 A/Accession: J05081
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-463 <CAL>
 A/Cross-references: EMBL:Z7133
 C/Comment: This protein is an intermembrane protein with seven transmembrane domains. It C/Genetics:
 A/Map position: 14
 C/Superfamily: presentin
 C/Keywords: transmembrane protein
 F/78-96/Domain: transmembrane #status predicted <TM1>
 F/129-150/Domain: transmembrane #status predicted <TM2>
 F/160-181/Domain: transmembrane #status predicted <TM3>
 F/191-209/Domain: transmembrane #status predicted <TM4>
 F/217-234/Domain: transmembrane #status predicted <TM5>
 F/240-257/Domain: transmembrane #status predicted <TM6>
 F/404-424/Domain: transmembrane #status predicted <TM7>

Query Match 93.5%; Score 2236; DB 2; Length 463;
 Best Local Similarity 93.8%; Pred. No. 1.5e-166;
 Matches 438; Conservative 12; Mismatches 13; Indels 4; Gaps 1;

Qy 1 MTEIPAPLSYFQNAQMSQNDNLSTVRSQNDREORNDRESLGHPPLSNGRPOGNSR 60
 Db 1 MTEIPAPLSYFQNAQMSQNDNLSTVRSQNDREORNDRESLGHPPLSNGRPOGNSG 56
 Qy 61 QVEODEEEDDELLTKYGAHYIMLFPVPTLCMVVVVATIKSVSPYTRKDGQILYTPFTE 120
 Db 57 PVVERDEDEDELLTKYGAHYIMLFPVPTLCMVVVVATIKSVSPYTRKDGQILYTPFTE 116
 Qy 121 DTEWQGRALSHSLNAAIMISIVVMTLLVLYKYCYKTHAMLISSILLFFESFI 180
 Db 117 DTEWQGRALSHSLNAAIMISIVVMTLLVLYKYCYKTHAMLISSILLFFESFI 176
 Qy 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYIKY 240
 Db 177 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYIKY 236
 Qy 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERNETLFPALIIYSTVWMLVNMME 300
 Db 237 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERNETLFPALIIYSTVWMLVNMME 296
 Qy 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEEMEAQDSHLGPHRSTESRAA 360
 Db 297 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEEMEAQDSHLGPHRSTESRAA 356
 Qy 361 VQELSSSILTAGEDPEERGVKLGDFIFYSYLVGASATASADMNTTIIACFVAIIIGLCL 420
 Db 357 VQELSSSILTAGEDPEERGVKLGDFIFYSYLVGASATASADMNTTIIACFVAIIIGLCL 416
 Qy 421 TLLLAIFKKALPALPISITFGLVFATDYLVQPFMDQLAFHQFYI 467
 Db 417 TLLLAIFKKALPALPISITFGLVFATDYLVQPFMDQLAFHQFYI 463

RESULT 5
 I78388
 S182 protein - mouse

C/Species: Mus musculus (house mouse)

C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999

C/Accession: I78388

R/Sherrington, R.; Rogae, E.; Liang, Y.; Rogae, E.A.; Levesque, G.; Ikeda, M.; Chi
 ero, I.; Pines, L.; Nee, L.; Chumakov, I.; Follen, D.; Brookes, A.; Sasseau, P.; Polt
 E.; Romenes, U.M.; St George-Hyslop, P.H.
 Nature 375, 754-760, 1995

A/Title: Cloning of a gene bearing missense mutations in early-onset familial Alzheimer
 A/Reference number: 158095; MUID:95319502; PMID:756406

A/Accession: I78388

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-467 <RES>

A/Cross-references: GB:I42177; NID:9904129; PIDN:AA62094.1; PID:9904130

C/Superfamily: presentin

Query Match 93.2%; Score 2228; DB 2; Length 467;
 Best Local Similarity 92.3%; Pred. No. 6.5e-166;
 Matches 431; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTEIPAPLSYFQNAQMSQNDNLSTVRSQNDREORNDRESLGHPPLSNGRPOGNSR 60
 Db 1 MTEIPAPLSYFQNAQMSQNDNLSTVRSQNDREORNDRESLGHPPLSNGRPOGNSR 60
 Qy 61 QVEODEEEDDELLTKYGAHYIMLFPVPTLCMVVVVATIKSVSPYTRKDGQILYTPFTE 120
 Db 61 QVEODEEEDDELLTKYGAHYIMLFPVPTLCMVVVVATIKSVSPYTRKDGQILYTPFTE 120
 Qy 121 DTEWQGRALSHSLNAAIMISIVVMTLLVLYKYCYKTHAMLISSILLFFESFI 180
 Db 122 DTEWQGRALSHSLNAAIMISIVVMTLLVLYKYCYKTHAMLISSILLFFESFI 180
 Qy 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYIKY 240
 Db 181 YLGEVFKTYNAVDTITVALLINFGVGMISIMKGPRLQQAALIMISALMALVFYIKY 240
 Qy 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERNETLFPALIIYSTVWMLVNMME 300
 Db 241 LPEWTAMLLIAYISYDVAVALCLKGPLRLMVEVTAQERNETLFPALIIYSTVWMLVNMME 300
 Qy 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEEMEAQDSHLGPHRSTESRAA 360
 Db 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEEMEAQDSHLGPHRSTESRAA 360
 Qy 361 VQELSSSILTAGEDPEERGVKLGDFIFYSYLVGASATASADMNTTIIACFVAIIIGLCL 420
 Db 361 VQELSSSILTAGEDPEERGVKLGDFIFYSYLVGASATASADMNTTIIACFVAIIIGLCL 420
 Qy 421 TLLLAIFKKALPALPISITFGLVFATDYLVQPFMDQLAFHQFYI 467
 Db 421 TLLLAIFKKALPALPISITFGLVFATDYLVQPFMDQLAFHQFYI 467

RESULT 6

JC5390

presentin-alpha - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C/Accession: J05390

R/Tsujiyama, A.; Yasojima, K.; Hashimoto-Gotoh, T.

Biochem. Biophys. Res. Commun. 231, 392-396, 1997

A/Title: Cloning of Xenopus presentin-alpha and -beta cDNAs and their differential exp

A/Reference number: J05390; MUID:97223465; PMID:9070286

A/Accession: J05390

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-433 <TSU>

A/Cross-references: DDBJ:D84427; NID:91944353; PIDN:BA19570.1; PID:91944354

A/Experimental source: brain

C/Comment: This protein plays a role in negative regulation of apoptotic cascades during

F/48-66/Domain: transmembrane #status predicted <TM1>
 F/99-119/Domain: transmembrane #status predicted <TM2>

F,130-143/Domain:	transmembrane	#status	predicted	<TM3>
F,161-178/Domain:	transmembrane	#status	predicted	<TM4>
F,187-203/Domain:	transmembrane	#status	predicted	<TM5>
F,210-227/Domain:	transmembrane	#status	predicted	<TM6>
F,374-394/Domain:	transmembrane	#status	predicted	<TM7>

Query Match	75.3%	Score 1801	DB 2	Length 433
Best Local Similarity	82.8%	Pred. No. 1,1e-132		
Matches 355; Conservative	26	Mismatches 48	Indels 0	Gaps 0

QY	39	IDRESLSLGPPELNSRPGCNSROVYEODEEDEDLTLKYGAHYMLFVPTLCMVVVVA	98
Db	5	SEBSNSENSECSNQOTSSSQVLBQDEEBDEBLTKYGAHYMLFVPTLCMVVVVA	64
QY	99	TIKSYSPYTRDQGLIYTPTEDETEYVQARLHSLINAINISVILVWTLILVYLXYRC	158
Db	65	TIKSYSPYTRDQGLIYTPTEDETESVQARLNSILNATIMISVILVWTLILVYLXYRC	124
QY	159	KYVHAMLISSLLIFFFSYILGEVKTNNVADYITVALLINPBGVGMISLHWGP	218
Db	125	KYVHGMWLISSLLIFFFSYIYLGVEKTYNVAADYITLMLLWNFVGMICHWNGP	184
QY	219	LRLQAYLIMISALMALVFIKYLPEWTAMLIYAVSYVDLVAVILCKKPLMLVETAOER	278
Db	165	LJLQOAYIIMISALMALVFIKYLPEWTMLLVAISYVDLVAVLSPKPLMLVETAOER	244
QY	279	NETLFPALISYSTWVLVWNAEGDPEAQRVSKNSKHAESTERESQDTVAENDDGGSF	338
Db	245	NETLFPALISYSTWIMLVWNAADGPGILKQASSTKYVNCAPTAPRSPASASDNGGPDY	304
QY	339	EMEQROSHLCPHRSTPESRAVQELSSILAGEDPERGKYLIGDGIIFYSLVGTASA	398
Db	305	TWEHRNQIOPINSTPESRAVQALPENSPESEPERGKYLIGDGIIFYSLVGTASA	364
QY	399	TASGDWNTLACFAVAILGLCTLILLALFKKALPALDISITFGLVFFAYDYLVQPEMD	458
Db	365	TASGDWNTLACFAVAILGLCTLILLALFKKALPALDISITFGLVFFAYDYLVQPEMD	424
QY	459	QLAFHQFYI 467	
Db	425	QLAFHQFYI 433	

RESULT 7
S63684
presentin11n_1, splice form 374 - human
N:Alternate names: Alzheimer's disease protein 3
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C:Accession: S63684
R:Salary, N.; Yahagi, Y.; Takagi, H.; Kondo, T.; Okochi, M.; Usami, M.; Shiraawa, T.; N
FEBS Lett. 381, 7-11, 1996
A:Title: Identification and characterization of presentin I-467, I-463 and I-374.
A:Reference number: S63683; MUID:96193501; PMID:8641442
A:Accession: S63684
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-374 <SAH>
A:Cross-references: EMBL:U40380; NID:g1244639; PIDN:AAB05895.1; PID:g1244640
C:Genetics:
A:Gene: GDB:PSEN1, AD3; FAD; S182; PS1
A:Cross-references: GDB:135662; OMIM:104311
A:Map position: 14q24.3-14q24.3
A:Superfamily: presentin11n

```

Query March      56.2% Score 1584; DB 2; Length 374;
Best Local Similarity 98.1%; Pseed 7.6e-116;
Matches 312; Conservative 1; Mismatches 1; Indels 4; Gaps 1

Cy 1 MTELPLPSTYPQNAQMSNDNLSTNTVRSQNDNRHREHDEHRRSLGHDPEPLSNRPGQNSR 60
bb 1 MTELPLPSTYPQNAQMSNDNLSTNTVRSQNDNRHREHDEHRRSLGHDPEPLSNRPGQNSR 56

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QY	6	QVVEQDEEBEDELTKYGAKHVIM.FVEVTLQVVVAATISVSFYRKQGLIYPETE	120
QY	57	QVVEQDEEBEDELTKYGAKHVIM.FVEVTLQVVVAATISVSFYRKQGLIYPETE	116
QY	121	DTETVQQRALHSILNNAIMISIVYVMTLLVLVLYKRCYKIHAMLISSLLFFESFI	180
Db	117	DTETVQQRALHSILNNAIMISIVYVMTLLVLVLYKRCYKIHAMLISSLLFFESFI	176
QY	181	YLAEVKRTNVAVDYTVALLFMNCGVGMISIMKGPRLQCAVILMISALMAVETKY	240
Db	177	YLAEVKRTNVAVDYTVALLFMNCGVGMISIMKGPRLQCAVILMISALMAVETKY	236
QY	241	LPENTAMILLIAVISYVDLVAVLCLXGPLRMLVETAOENETLLFPALLYSSTMVLVNNAE	300
Db	237	LPENTAMILLIAVISYVDLVAVLCPXGPLRMLVETAOENETLLFPALLYSSTMVLVNNAE	296
QY	301	GDEPAQRVSKSKSNNAE 318	
Db	297	GDEPAQRVSKSKSNNAE 314	

RESULT 8
Jc5391
presenilin-beta - African clawed frog
C|Species: Xenopus laevis (African clawed frog)
C|Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C|Accession: Jc5391
R|Tsujimura, A.; Yasojima, K.; Hashimoto-Goth, T.
Biochem. Biophys. Res. Commun. 231, 392-396, 1997
A|Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and their differential exp
A|Reference number: Jc5390; MUID:972223465; PMID:9070286
A|Accession: Jc5391
A|Status: nucleic acid sequence not shown
A|Molecule type: mRNA
A|Residues: 1-449 <TSU>
A|Cross-references: DDBJ:D84428; NID:G194435; PIDN:BAA19571.1; PID:G1944356
A|Experimental source: brain
C|Comment: This protein plays a role in negative regulation of apoptotic cascades durin
C|Superfamily: presenilin
F:91-109/Domain: transmembrane #status predicted <TM1>
F:143-167/Domain: transmembrane #status predicted <TM2>
F:173-192/Domain: transmembrane #status predicted <TM3>
F:204-221/Domain: transmembrane #status predicted <TM4>
F:230-246/Domain: transmembrane #status predicted <TM5>
F:252-279/Domain: transmembrane #status predicted <TM6>
F:390-410/Domain: transmembrane #status predicted <TM7>

Query Match	61.2%	Score 1462.5	DB 2	Length 449
Best Local Similarity	64.1%	Pred. No. 2.8e-106		
Matches 302; Conservative	47;	Mismatches 75;	Indels 47;	Gaps 7

QY TELPAPLASYFONAKMSDEHSLNTRVRSQNDNREKHNDRLSLGHPPLNENGBOG----- 57
 Db 21 SESEPPLSYQDQVQNSGEGLETYS-----HRENGPQSTQNN-----EDVENGTSGDAY 69
 QY 58 NSRQVYEQDEBEDEBELTLKYGAKYIMLPVYTLQWYVATISVSFFYTRKQGLITP 117
 Db 70 NSERTV--EENESEBELTLKYGARHITMFPVTLQWYVATISVSFFYTRKQGLITP 126
 QY 118 FTEDTETVQGRALSHLNAIMISYIVMTLLVLYKYRCYKIHAMLISLTLFFF 177
 Db 127 FSEDTSVSGRLNLSVNTLIMISVILMTFTLVLVLYRCYKIHMLISLTLFME 186
 QY 178 SFYLGSEFTYVAVDYTYVALLIMNGGVGMISIHKGELRFQQAYLIMISALMALVE 237
 Db 187 TYILSEVFRTINADYPTLFTLWNGGAMGICHHKGPLOQQAYLIMISALMALVE 246
 QY 238 IKTLPEMTAMLIAYSTYDLVAYTCLKGPLRMLVTRQENBELPALYSSMTMLVN 297
 Db 247 IKTLPEMSAVILGALSYVDLVAICPQGPLRMLVTRQENBELPALYSSAMTMYG 306
 QY 298 MAEGDEAQRVYSKSKKHNASTEREESODTYAENDDGGFSEWEAQRDLSHLPGRSTPES 357

Db 307 MAD-SATADGRMNQOVCHIDNTEGANSIV-----ED 338
 QY 358 RAAVOELSSSIAGEDP-EERGVKLGIDPFYSVLVGKASATASGDMNTTICFAVAIL 416
 Db 339 AAEIRICQUSLSEBDEPERGVKLGIDPFYSVLVGKAAATSGDMNTTICFAVAIL 398
 QY 417 GLCITLLALLAFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 467
 Db 399 GLCITLLALLAFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 449

RESULT 9

presentin 2 - human
 A:Accession: A56993
 C:Species: Homo sapiens (man)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Nov-2000
 C:Accession: A56993; 158098
 R:Levy-Lahad, E.; Maeco, W.; Poorkaj, P.; Romano, D.M.; Oshima, J.; Pettingell, W.H.; Yu
 Science 269, 973-977, 1995
 A:Title: Candidate gene for the chromosome 1 familial Alzheimer's disease locus.
 A:Reference number: A56993; PMID:95365816; PMID:7638622
 A:Accession: A56993
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-448 <RES>
 A:Cross-references: GB:L43964; NID:G951202; PIDN:AAB59557.1; PID:G951203
 R:Rogaev, E.I.; Sherrington, R.; Rogaeva, E.A.; Levesque, G.; Ikeda, M.; Liang, Y.; Chi,
 ; Cohen, D.; Lannfelt, L.; Fraser, P.E.; Rommens, J.M.; St George-Hyslop, P.H.
 Nature 376, 775-778, 1995
 A:Title: Familial Alzheimer's disease in kindreds with missense mutations in a gene on C
 A:Reference number: 158098; MUID:95379971; PMID:7651536
 A:Accession: 158098
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122; P:124-448 <RES>
 A:Cross-references: GB:L44577; NID:G950347; PIDN:AAC42012.1; PID:G950348
 C:GeneticS:
 A:Gene: GDB:PSEN2; ADA; STM2; PS2; ES-1
 A:Cross-references: GDB:633044; OMIM:600759
 A:Map position: 1q31-1q42
 C:Superfamily: presentin

Query Match 60.4%; Score 1444; DB 2; Length 448;
 Best Local Similarity 65.0%; Pred. No. 7.6e-15; Indels 42; Gaps 8;
 Matches 303; Conservative 40; Mismatches 81; GRPG-----
 QY 3 ELPAISYQNAQMSDNHLSNTVRSQNDNRQENHNR-SLGHPEPLSNRPGNSRQ 61
 Db 24 EEPFRSCQEGRGQPEDENTAQRSGENEDGEDPDRYVCSGV-----GRPG----- 74
 QY 62 VVEQDEBDEDELTKYGAHVIMLFPVPTLCMVVVVATIKSVSYTRKQGLIYPTFTD 121
 Db 75 -----LEEBLTKYGAHVIMLFPVPTLCMVVVVATIKSVSYTRKQGLIYPTFTD 127
 QY 122 TETVGRALHSILNAAMISVIVMTLLVLYKRCYKVHAWLIISLLFFESFIY 181
 Db 128 TFSVGRLLNSVLTMLMISIVMTIFIVLVLYKRCYKFIHGLIMSLMLFFIY 187
 QY 182 LGSEVKTNNVAVDYITVALIINFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 241
 Db 188 LGSEVKTNNVAVDYITVALIINFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 247
 QY 242 PENTAMILLIAVSYVDVAVCLKGPLMLVETAQENETLFPALIVSTWMLVMAEG 301
 Db 248 PEMSAMVILGALSYVDVAVCLKGPLMLVETAQENETLFPALIVSTWMLVMAEG 307
 QY 302 DPBAQRVSKSKNAESTERESQDTVAENDGCFSEMEARQDSHLGPHRSTPESRAV 361
 Db 308 DPBSQGLAL-CLPYDPE-MEEDSYDSFGE--PSYVPEFPPPLNGYPG-----349
 QY 362 QELSSSIAGDEPBERGVKLGIDPFYSVLVGKASATASGDMNTTICFAVAILGCLT 421
 Db 362 QELSSSIAGDEPBERGVKLGIDPFYSVLVGKASATASGDMNTTICFAVAILGCLT 421

Db 350 EEL-----EERERGVKLGIDPFYSVLVGKAAATSGDMNTTICFAVAILGCLT 402
 QY 422 LLLLAIFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 467
 Db 403 LLLLAIFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 448

RESULT 10

seven trans-membrane domain protein AD3LP/ADS - human
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 29-Sep-1999
 C:Accession: I39174
 R:Li, J.; Ma, J.; Potter, H.
 Proc. Natl. Acad. Sci. U.S.A. 92, 12180-12184, 1995
 A:Title: Identification and expression analysis of a potential familial Alzheimer's dis
 A:Reference number: I39174; MUID:96109229; PMID:8618867
 A:Accession: I39174
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-442 <RES>
 A:Cross-references: EMBL:U34349; NID:G1079575; PIDN:AAC50290.1; PID:G1079576
 C:Superfamily: presentin

Query Match 57.6%; Score 1376.5; DB 2; Length 442;
 Best Local Similarity 63.7%; Pred. No. 1.4e-99;
 Matches 286; Conservative 40; Mismatches 82; Indels 41; Gaps 6;
 QY 3 ELPAISYQNAQMSDNHLSNTVRSQNDNRQENHNR-SLGHPEPLSNRPGNSRQ 61
 Db 24 EEPFRSCQEGRGQPEDENTAQRSGENEDGEDPDRYVCSGV-----GRPG----- 74
 QY 62 VVEQDEBDEDELTKYGAHVIMLFPVPTLCMVVVVATIKSVSYTRKQGLIYPTFTD 121
 Db 75 -----LEEBLTKYGAHVIMLFPVPTLCMVVVVATIKSVSYTRKQGLIYPTFTD 127
 QY 122 TETVGRALHSILNAAMISVIVMTLLVLYKRCYKVHAWLIISLLFFESFIY 181
 Db 128 TFSVGRLLNSVLTMLMISIVMTIFIVLVLYKRCYKFIHGLIMSLMLFFIY 187
 QY 182 LGSEVKTNNVAVDYITVALIINFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 241
 Db 188 LGSEVKTNNVAVDYITVALIINFGVGMISIMKGPLRQOAVLIMISALMALVFIKYL 247
 QY 242 PENTAMILLIAVSYVDVAVCLKGPLMLVETAQENETLFPALIVSTWMLVMAEG 301
 Db 248 PEMSAMVILGALSYVDVAVCLKGPLMLVETAQENETLFPALIVSTWMLVMAEG 307
 QY 302 DPBAQRVSKSKNAESTERESQDTVAENDGCFSEMEARQDSHLGPHRSTPESRAV 361
 Db 308 DPBSQGLAL-----PYDPEMEDSYDSFGEPSYVPEFPPPLNGYPG-----348
 QY 362 QELSSSIAGDEPBERGVKLGIDPFYSVLVGKASATASGDMNTTICFAVAILGCLT 421
 Db 349 EELER-----EESQSGVYLGIDPFYSVLVGKAAATSGDMNTTICFAVAILGCLT 403
 QY 422 LLLLAIFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 467
 Db 404 LLLLAIFKALPALPISITFGIVFPAYDYLQVPMQJAFHOPI 448

RESULT 11

protein F35H12.3 (imported) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
 C:Accession: E89453
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C. ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:50:51 / Search time 17 Seconds

(without alignments)
1430.398 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391
Sequence: 1 MTELPAPLSYFGNAQMSDN.....ATDYLVPPMDQLARHGFYI 467

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	99.5	467	1 PSN1_HUMAN	P49768 homo sapien
2	2354	98.5	467	1 PSN1_MACFA	Q8HW55 macaca fasc
3	2266	94.8	467	1 PSN1_MICMU	P79802 microcebus
4	2228	93.2	467	1 PSN1_MOUSE	P49769 mus musculu
5	2200.5	92.0	468	1 PSN1_RAT	P97887 rattus norv
6	2175.5	91.0	478	1 PSN1_BOVIN	Q9X977 bos taurus
7	1801	75.3	433	1 PSN1_XENLA	O12976 xenopus lae
8	1614.5	67.5	456	1 PSN1_BRAKE	Q9W6C7 brachydact
9	1462.5	61.2	449	1 PSN2_XENLA	O12977 xenopus lae
10	1452	60.7	448	1 PSN2_HUMAN	P49810 homo sapien
11	1440	60.2	445	1 PSN2_MICMU	P79801 microcebus
12	1432.5	59.9	449	1 PSN2_BOVIN	Q9X996 bos taurus
13	1430	59.8	448	1 PSN2_RAT	Q88777 rattus norv
14	1428	59.7	448	1 PSN2_MOUSE	O61144 mus musculu
15	1415	59.2	441	1 PSN2_BRAKE	Q90764 brachydact
16	1174.5	49.1	441	1 PSN1_DROME	O02194 drosophila
17	1054.5	44.1	444	1 PSN1_CAEEL	P52166 caenorhabdi
18	539.5	22.6	453	1 PSN1_ARATH	O64668 arabidopsis
19	538	22.5	397	1 PSN3_ARATH	Q9S1K7 arabidopsis
20	505	21.1	358	1 HOP1_CAEEL	O02100 caenorhabdi
21	309.5	12.9	465	1 SPFA_CAEEL	O01608 caenorhabdi
22	120.5	5.0	2386	1 RAD3_SCHPO	O02099 schizosacch
23	117	4.9	601	1 OAR_DROME	P22370 drosophila
24	114.5	4.8	323	1 CD47_HUMAN	Q08722 homo sapien
25	108.5	4.5	971	1 Y277_WYCPN	P75387 mycoplasma
26	107.5	4.5	2365	1 CCAH_MOUSE	O88427 mus musculu
27	107.5	4.5	488	1 YB91_YEAST	P38142 saccharomyc
28	106.5	4.5	436	1 A2AR_CARAU	P32251 carassius a
29	104	4.3	520	1 PSU2_HUMAN	O88C68 homo sapien
30	103.5	4.3	354	1 C3X1_MOUSE	O92069 mus musculu
31	102	4.3	713	1 ACCH_HUMAN	O18007 caenorhabdi
32	102	4.3	1580	1 ACCH_HUMAN	Q09428 homo sapien
33	101.5	4.2	754	1 YCA1_ECOLI	P37443 escherichia

34	101	4.2	441	1 DIHR_ACHDO	Q16983 acheta dome
35	101	4.2	519	1 ACH4_DROME	P25162 drosophila
36	101	4.2	672	1 HYFB_ECOLI	P23482 escherichia
37	100.5	4.2	1492	1 CFTF_SQUAC	P23652 squatus aca
38	100	4.2	1581	1 ACC6_RAT	O09429 rattus norv
39	100	4.2	2144	1 CDR2_RAT	Q94922 rattus norv
40	99.5	4.2	628	1 YS9A_CAEEL	O96060 caenorhabdi
41	99.5	4.2	1985	1 CCAF_MOUSE	Q9167 mus musculu
42	99	4.1	347	1 UL33_HSVGU	P52380 human herpe
43	99	4.1	512	1 YMO9_MYCTU	Q10398 mycobacteri
44	98	4.1	1558	1 YK83_YEAST	P36028 saccharomyc
45	97.5	4.1	855	1 PT13_ARATH	Q81P18 arabidopsis

ALIGNMENTS

RESULT 1
PSN1_HUMAN STANDARD, PRT, 467 AA.
ID PSN1_HUMAN Q55465; Q14762; Q15719; Q15720; Q66P33; Q9UIF0;
AC P49768; O55465; Q14762; Q15719; Q15720; Q66P33; Q9UIF0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Presentin 1 (PS-1) (S182 protein).
GN PSN1 OR PSN1 OR AD3 OR PS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS AD3.
RC Tissue:Brain;
RA MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogava E.I., Liang Y., Rogava E.A., Levesque G.,
RA Ikeda M., Chi H., Lin C., Li G., Holman K., Tenda T., Mar L.,
RA Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainone I.,
RA Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA Samsen P., Polinsky R.J., Masco W., da Silva H.A.R., Haines J.L.,
RA Perlick-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Romenes J.M., St George-Hyslop P.H.;
RA "Cloning of a gene bearing missense mutations in early-onset familial
RA Alzheimer's disease.";
RL Nature 375:754-760(1995).
[2]
SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC Tissue:Blood and Brain;
RA MEDLINE=96193901; PubMed=8641442;
RA Sahara N., Yahagi Y.-I., Takagi H., Kondo T., Okochi M., Usami M.,
RA Shirasawa T., Mori H.;
RA "Identification and characterization of presentin I-467, I-463 and
RA I-374.";
RL FEBS Lett. 381:7-11(1996).
[3]
SEQUENCE FROM N.A. (ISOFORM 4).
RA Powell C.S., Gegg M.E., Palmer M.S.;
RA "Human presentin 1 gene encodes an alternative protein-minilin.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A. (ISOFORM 5).
RA Kang L., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Doris M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Laszy S., Hood L.;
RT "Complete sequence of the gene for presentin 1.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RA PubMed=12508121;
RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,
RA Cattoi L., Levy M., Barde V., De Bernardis V., Ureta-Vidal A.,

- RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
 RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Craud C.,
 RA Brule T., Vailion O., Friedlander L., Samson G., Broctier P.,
 RA Cure S., Segreus B., Aniere P., Samain S., Crespeau H., Abbaei N.,
 RA Aitch N., Boscus D., Dickhoff R., Dors M., Dubois I., Fiedman C.,
 RA Gouyennoux M., James R., Madan A., Maity-Satradra B., Mangano S.,
 RA Martins N., Menard M., Ozas S., Ratcliffe A., Shaffer T., Trask B.,
 RA Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,
 RA Batoli-Marel D., Bourard M., Briez-Silla S., Combette S.,
 RA Dutoise-Laurent V., Ferron C., Lechaplais C., Louesse C., Muelet D.,
 RA Magdelenat G., Pateau E., Petit E., Sirvain-Trukhlewicz P., Trybou A.,
 RA Vega-Carraz N., Bataille E., Bluet E., Bortelais I., Dubois M.,
 RA Dumont C., Gerin T., Haflray S., Hammadi R., Munga J., Pellicouin V.,
 RA Robert D., Wundler E., Gauguet G., Roy A., Sainte-Marthe L.,
 RA Verdier J., Verdier-Discala C., Hillier L.M., Fulton L., McPherson J.,
 RA Masuda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,
 RA Queller F., Waterston R., Hood L., Weissbach J.,
 RT "The DNA sequence and analysis of human chromosome 14." ,
 RL Nature 421:601-607(2003).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Skin;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheer T.E.,
 RA Brownstein W.J., Ueda T.B., Tomshiki S., Canninci P., Prange C.,
 RA Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gundacker P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodigues R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ,
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 1-113 FROM N.A.
 RA Tsujimura A., Hashimoto-Gotoh T.,
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=96160372; PubMed=8574969;
 RA Kovacs D.M., Fausett H.J., Page K.J., Kim T.-W., Moir R.D.,
 RA Meriam D.E., Hollister R.D., Hallmark O.G., Mancini R.,
 RA Felsenstein K.W., Hyman B.T., Tanzi R.E., Masco W.,
 RT "Alzheimer-associated presenilin 1 and 2: neuronal expression in
 RT brain and localization to intracellular membranes in mammalian
 RT cells." ,
 RL Nat. Med. 2:224-229(1996).
 RN [10]
 RP PROCESSING
 RX MEDLINE=9317150; PubMed=9173929;
 RA Podlasky W.B., Citron M., Amaratne P., Sherrington R., Xia W.,
 RA Zhang J., Diehl T., Levesque G., Fraser P., Haass C., Koo B.H.,
 RA Schubert P., St George-Hyslop P., Teplow D.B., Selkoe D.J.,
 RT "Presenilin proteins undergo heterogeneous endoproteolysis between
 RT Thr91 and Ala299 and occur as stable N- and C-terminal fragments in
 RT normal and Alzheimer brain tissue." ,
 RL Neurobiol. Dis. 3:325-337(1997).
 RN [11]
 RP FUNCTION, AND MUTAGENESIS OF MET-292.
 RX MEDLINE=20014554; PubMed=10545183;
 RA Steiner H., Romig H., Pasold B., Philipp U., Baader M., Citron M.,
 RA Loeschner H., Jacobsen H., Haass C.,
 RT "Amyloidogenic function of the Alzheimer's disease-associated
 RP Presenilin 1 in the absence of endoproteolysis." ,
 RT Biochemistry 38:14600-14605(1999).
 RN [12]
 RP FUNCTION.
 RX MEDLINE=20062913; PubMed=10593990;
 RA Ray W.J., Yao M., Mumm J., Schroeder E.H., Safirig P., Wolfe M.,
 RA Selkoe D.J., Kopan R., Goate A.M.,
 RT "Cell surface presenilin-1 participates in the gamma-secretase-like
 RT proteolysis of Notch." ,
 RL J. Biol. Chem. 274:36801-36807(1999).
 RN [13]
 RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
 RX MEDLINE=99221485; PubMed=10206644;
 RA Wolfe M.S., Xia W., Ostaszewski B.L., Diehl T.S., Kimberly W.T.,
 RA Selkoe D.J.,
 RT "Two transmembrane aspartates in presenilin-1 required for presenilin
 RT endoproteolysis and gamma-secretase activity." ,
 RL Nature 398:513-517(1999).
 RN [14]
 RP FUNCTION, AND MUTAGENESIS OF ASP-257 AND ASP-385.
 RX MEDLINE=20359495; PubMed=10899933;
 RA Berzovska O., Jack C., McLean P., Aster J.C., Hicks C., Xia W.,
 RA Wolfe M.S., Kimberly W.T., Weinmaster G., Selkoe D.J., Hyman B.T.,
 RT "Aspartate mutations in presenilin and gamma-secretase inhibitors both
 RT impair notch proteolysis and nuclear translocation with relative
 RT preservation of notch signaling." ,
 RL J. Neurochem. 75:583-593(2000).
 RN [15]
 RP FUNCTION, AND MUTAGENESIS OF LEU-286.
 RX MEDLINE=20283925; PubMed=10811883;
 RA Kulic L., Walter J., Multhaup G., Teplow D.B., Baumeister R.,
 RA Romig H., Capell A., Steiner H., Haass C.,
 RT "Separation of presenilin function in amyloid beta-peptide generation
 RT and endoproteolysis of Notch." ,
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5913-5918(2000).
 RN [16]
 RP FUNCTION.
 RX PubMed=11226248;
 RA Bakt L., Marandaud P., Efthimiopoulos S., Georgakopoulos A., Wen P.,
 RA Cui W., Shioi U., Koo E., Osawa M., Friedrich V.L., Robakis N.K.,
 RT "Presenilin-1 binds cytoplasmic epithelial cadherin, inhibits
 RT cadherin/p120 association, and regulates stability and function of
 RT the cadherin/catenin adhesion complex." ,
 RL Proc. Natl. Acad. Sci. U.S.A. 98:2381-2386(2001).
 RN [17]
 RP INTERACTIONS WITH F1NA AND F1NB.
 RX MEDLINE=98099802; PubMed=9437013;
 RA Zhang W., Han S.W., McKee D.W., Goate A., Wu J.Y.,
 RT "Interaction of presenilin with the filament family of actin-binding
 RT proteins." ,
 RL J. Neurosci. 18:914-922(1998).
 RN [18]
 RP INTERACTION WITH DELTA-2 CATELIN.
 RX MEDLINE=99155075; PubMed=10037471;
 RA Levesque G., Yu G., Nishimura M., Zhang D.M., Levesque L., Yu H.,
 RA Xu D., Liang Y., Kogaeva E., Ikeda W., Dutche M., Murgolo N., Wang L.,
 RA Vanderveer P., Bayne M.L., Strader C.D., Rommens J.M., Fraser P.B.,
 RA St George-Hyslop P.,
 RT "Presenilins interact with armadillo proteins including
 RT neural-specific plakophilin-related protein and beta-catenin." ,
 RL J. Neurochem. 72:999-1008(1999).
 RN [19]
 RP INTERACTION WITH HERPUD1.
 RX MEDLINE=21935377; PubMed=11799129;
 RA Sai X., Kawamura Y., Kokame K., Yamaguchi H., Shiraiishi H., Suzuki R.,
 RA Suzuki T., Kawachi M., Miyata T., Kitamura T., De Strooper B.,
 RA Yanagisawa K., Komano H.,
 RT "Endoplasmic reticulum stress-inducible protein, Herp, enhances
 RT presenilin-mediated generation of amyloid beta-protein." ,
 RL J. Biol. Chem. 277:12915-12920(2002).
 RN [20]
 RP COMPONENT OF A GAMMA-SECRETASE COMPLEX WITH PEN2, PSEN1/PSEN2 AND
 RP NCSTN.

Query Match 99.5%; Score 2378; DB 1; Length 467;
 Best Local Similarity 99.6%; Pred. No. 3,1e-156;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSQEDNHLSTNTRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSTYFQNAQMSQEDNHLSTNTRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
 QY 61 QVEODEEEDBELTLKYGAKVIMLFVPTLCMVVAVATIKSVFYTRKDGQILYTPFTE 120
 DB 61 QVEODEEEDBELTLKYGAKVIMLFVPTLCMVVAVATIKSVFYTRKDGQILYTPFTE 120
 QY 121 DTEYVGRALHSLINAAIMISVIVMTLLVLYKRCYKHYHMLIISLLFFESFI 180
 DB 121 DTEYVGRALHSLINAAIMISVIVMTLLVLYKRCYKHYHMLIISLLFFESFI 180
 QY 121 YLGEVFKTYNVAVDITVALLINFGVGMISIMHKGRLQQAYLIMISALMALVFIRY 240
 DB 121 YLGEVFKTYNVAVDITVALLINFGVGMISIMHKGRLQQAYLIMISALMALVFIRY 240
 QY 241 LPEWTAMLIIVISYDVAVALCKGRLMLVETAOENETLFPALITYSTWVLVMAE 300
 DB 241 LPEWTAMLIIVISYDVAVALCKGRLMLVETAOENETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAGRVSKSKNAESTERESODTYAENDGGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDEPAGRVSKSKNAESTERESODTYAENDGGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALIGLCL 420
 QY 421 TLLILAIFKALPALPISITTEGLVFYFATDYLVOFMDQLAFHORYI 467
 DB 421 TLLILAIFKALPALPISITTEGLVFYFATDYLVOFMDQLAFHORYI 467

RESULT 2
 PSNI_MACFA STANDARD; PRT; 467 AA.
 ID PSNI_MACFA STANDARD; PRT; 467 AA.
 AC Q8HXM5;
 DT 10-OCT-2003 (Rel. 42; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Presentin 1 (PS-1).
 GN PSNI OR PSNI OR PSI.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OS Bakayotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CC NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Frontal cortex;
 RA Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.;
 RT "Isolation and characterization of cDNA for macaque neurological
 disease genes";
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. Regulates epithelial-
 cadherin function (By similarity).
 CC cadherin: Homodimer. Component of the gamma-secretase complex, a
 complex composed of a presenilin homodimer (PSEN1 or PSEN2),
 nicastrin (NCTN), APH1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Predominantly heterodimer of a N-terminal
 (NT) and a C-terminal (CT) endoproteolytic fragment.

CC Associates with proteolytic processed C-terminal fragments C83 and
 CC C99 of the amyloid precursor protein (APP). Associates with
 CC NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and
 CC plakophilin 4. Interacts with DOK3. Interacts with HHR23D1, FLNA
 CC and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Belongs to the presenilin family.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).

DR EMBL: AB083326; BAC20605.1; -
 DR Interpro: IPR006639; Peptidase_A22.
 DR Pfam: PF01080; Presenilin; 1.
 DR PRINTS: PRO1072; PRESENILIN.
 DR SMART: SM00730; PSN; 1.
 KM Transmembrane, phosphorylation; Endoplasmic reticulum; Golgi stack.
 FT CHAIN 1 298 PRESENILIN 1 NTF SUBUNIT (BY SIMILARITY).
 FT CHAIN 1 467 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
 FT TRANSMEM 83 103 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 244 264 POTENTIAL.
 FT TRANSMEM 408 428 POTENTIAL.
 FT TRANSMEM 433 453 POTENTIAL.
 FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 SQ SEQUENCE 467 AA; 52573 MW; 0D5E0ED73BE30F3 CRC64;

Query Match 98.5%; Score 2354; DB 1; Length 467;
 Best Local Similarity 98.6%; Pred. No. 1.5e-156;
 Matches 462; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSQEDNHLSTNTRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSTYFQNAQMSQEDNHLSTNTRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
 QY 61 QVEODEEEDBELTLKYGAKVIMLFVPTLCMVVAVATIKSVFYTRKDGQILYTPFTE 120
 DB 61 QVEODEEEDBELTLKYGAKVIMLFVPTLCMVVAVATIKSVFYTRKDGQILYTPFTE 120
 QY 121 DTEYVGRALHSLINAAIMISVIVMTLLVLYKRCYKHYHMLIISLLFFESFI 180
 DB 121 DTEYVGRALHSLINAAIMISVIVMTLLVLYKRCYKHYHMLIISLLFFESFI 180
 QY 121 YLGEVFKTYNVAVDITVALLINFGVGMISIMHKGRLQQAYLIMISALMALVFIRY 240
 DB 121 YLGEVFKTYNVAVDITVALLINFGVGMISIMHKGRLQQAYLIMISALMALVFIRY 240
 QY 241 LPEWTAMLIIVISYDVAVALCKGRLMLVETAOENETLFPALITYSTWVLVMAE 300
 DB 241 LPEWTAMLIIVISYDVAVALCKGRLMLVETAOENETLFPALITYSTWVLVMAE 300
 QY 301 GDEPAGRVSKSKNAESTERESODTYAENDGGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDEPAGRVSKSKNAESTERESODTYAENDGGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALIGLCL 420
 DB 361 VOELSSSILAGEDPEERGVKLGDFIFYSVLVGKASATASGDMNTTACFVALIGLCL 420

QY 421 TLLLAIFKKALPALPISITFGVVFATDYLVOPFMDQLAFHQFYI 467
 DB 421 TLLLAIFKKALPALPISITFGVVFATDYLVOPFMDQLAFHQFYI 467

RESULT 3
 PSN1 MICMU STANDARD; PRT; 467 AA.

ID PSN1 MICMU
 AC P79802;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presentin 1 (PS-1).
 GN PSN1 OR PSN1 OR PS1.
 OS Microcebus murinus (Lesser mouse lemur).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsitrhini; Cheirogaleidae;
 OC Microcebus.
 OC NCBI_TaxID=30608;
 RX SEQUENCE FROM N.A. (ISOFORMS I-463 AND I-467).
 RX TISSUE=Brain;
 RX MEDLINE=97079199; PubMed=8920931;
 RA Calenda A., Mestre-Frances N., Czech C., Pradier L., Bons N.,
 RA Bellis M.;
 RT "Molecular cloning, sequencing, and brain expression of the
 RT presentin 1 gene in Microcebus murinus";
 RL Biochem. Biophys. Res. Commun. 228:430-439 (1996).
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors and
 CC APP (beta-amyloid precursor protein). Requires the other members
 CC of the gamma-secretase complex to have a protease activity. May
 CC play a role in intracellular signaling and gene expression or in
 CC linking chromatin to the nuclear membrane. Regulates epithelial-
 CC cadherin function (By similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 CC complex composed of a presentin homodimer (PSN1 or PSN2), a
 CC nicastrin (NCSTN), Apha1 (Apha1 or Apha1B) and PSN2. Such minimal
 CC complex is sufficient for secretase activity, although other
 CC components may exist. Predominantly heterodimer of a N-terminal
 CC (NTP) and a C-terminal (CTP) endoproteolytic fragment.
 CC Associates with proteolytic processed C-terminal fragments C83 and
 CC C99 of the amyloid precursor protein (APP). Associates with
 CC NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and
 CC plakophilin 4. Interacts with DOK3. Interacts with HERPUD1, FLNA
 CC and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=I-467;
 CC IsoId=P79802-1; Sequence=Displayed;
 CC Name=I-463;
 CC IsoId=P79802-2; Sequence=VSP_005193;
 CC -1- TISSUE SPECIFICITY: Found predominantly in neurons of the
 CC different cortical layers and hippocampus but also in subcortical
 CC structures.
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Belongs to the presentin family.
 CC -----
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DR EMBL; Z71333; CAA95930.1; .
 DR PIR; JCS080; JCS080.
 DR PIR; JCS081; JCS081.
 DR MEROPS; A2.001; .

DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentin_1.
 DR PRINTS; PR01072; PRESENTIN.
 DR SMART; SM00730; PSN; 1.
 DR SMART; SMO0730; PSN; 1.
 DR Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack;
 KW Alternative splicing.
 FT CHAIN 1 298 PRESENTIN 1 NTF SUBUNIT (BY SIMILARITY).
 FT CHAIN 299 467 PRESENTIN 1 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 82 102 POTENTIAL.
 FT DOMAIN 103 132 LUMENAL (POTENTIAL).
 FT DOMAIN 133 153 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 161 181 LUMENAL (POTENTIAL).
 FT DOMAIN 182 190 LUMENAL (POTENTIAL).
 FT DOMAIN 191 211 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 212 220 POTENTIAL.
 FT DOMAIN 221 241 LUMENAL (POTENTIAL).
 FT DOMAIN 242 243 POTENTIAL.
 FT DOMAIN 244 264 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 265 407 POTENTIAL.
 FT TRANSMEM 408 428 POTENTIAL.
 FT TRANSMEM 433 453 POTENTIAL.
 FT SITE 291 292 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT SITE 292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE
 FT VARSPIC 26 29 Missing (in isoform I-463).
 FT FT Missing (in isoform I-463).
 FT FT Missing (in isoform I-463).
 SQ SEQUENCE 467 AA; 52384 MW; D966FF2CA782975C CRC64;

Query Match 94.8%; Score 2266; DB 1; Length 467;
 Best Local Similarity 94.6%; Pred. No. 1; 9e-150;
 Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTELPALPLSYFQNAQNSQEDHLSNTVRSQNDNREORHNDRSLSGHPPLSNRPGQNSR 60
 DB 1 MTELPALPLSYFQNAQNSQEDHLSNTVRSQNDNREORHNDRSLSGHPPLSNRPGQNSG 60

QY 61 QVVEQDEDEDEELTKYGANGVIMLFPVPTLCVAVVAVATKVSFYTRKDGOLITPPTF 120
 DB 61 PVVERDEDEDEELTKYGANGVIMLFPVPTLCVAVVAVATKVSFYTRKDGOLITPPTF 120

QY 121 DTEVGGORALHSITNAIMTSVIVMTILVLYKTRCVYTHAMLIISLLFFPSFI 180
 DB 121 DTEVGGORALHSITNAIMTSVIVMTILVLYKTRCVYTHAMLIISLLFFPSFI 180

QY 121 YLGEVFETYNVAVDYITVALLINFGVGMISIMKGPLRLQAYILMISALMALVFIFY 240
 DB 121 YLGEVFETYNVAVDYITVALLINFGVGMISIMKGPLRLQAYILMISALMALVFIFY 240

QY 181 YLGEVFETYNVAVDYITVALLINFGVGMISIMKGPLRLQAYILMISALMALVFIFY 240
 DB 181 YLGEVFETYNVAVDYITVALLINFGVGMISIMKGPLRLQAYILMISALMALVFIFY 240

QY 241 LPETAWLILAVISVYDLVAVLCLKGPRLVETAQRNETLPPALISSTWMLVMAE 300
 DB 241 LPETAWLILAVISVYDLVAVLCLKGPRLVETAQRNETLPPALISSTWMLVMAE 300

QY 241 LPETAWLILAVISVYDLVAVLCLKGPRLVETAQRNETLPPALISSTWMLVMAE 300
 DB 241 LPETAWLILAVISVYDLVAVLCLKGPRLVETAQRNETLPPALISSTWMLVMAE 300

QY 301 GDPFAQRRVSKNSKNNSTERSQDTVAENDDGSESEWEAQRDSHLPGRSTPSRAA 360
 DB 301 GDPFAQRRVSKNSKNNSTERSQDTVAENDDGSESEWEAQRDSHLPGRSTPSRAA 360

QY 301 GDPFAQRRVSKNSKNNSTERSQDTVAENDDGSESEWEAQRDSHLPGRSTPSRAA 360
 DB 301 GDPFAQRRVSKNSKNNSTERSQDTVAENDDGSESEWEAQRDSHLPGRSTPSRAA 360

QY 361 VQELSSSITLAGEDEBERGVLCGDPFFYGVNKGKASATSGGMNTTICFVALILGLCL 420
 DB 361 VQELSSSITLAGEDEBERGVLCGDPFFYGVNKGKASATSGGMNTTICFVALILGLCL 420

QY 421 TLLLAIFKKALPALPISITFGVVFATDYLVOPFMDQLAFHQFYI 467
 DB 421 TLLLAIFKKALPALPISITFGVVFATDYLVOPFMDQLAFHQFYI 467

RESULT 4
 PSN1 MOUSE STANDARD; PRT; 467 AA.
 ID PSN1 MOUSE
 AC P49769; Q91WK6; Q91LP9;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Presentin1 (P51-1) (S182 protein).

GN PSEN1 OR PSN1 OR AD3H.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=9531502; PubMed=7596406;

RA Sherrington R., Rogaeve E.I., Liang Y., Rogaeve E.A., Levesque G., Ikeda M., Chi H., Lin C., Li G., Holman K., Tenda T., Mar L., Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rajneo I., Pinessi L., Nee L., Chumakov I., Pollen D., Brooks A., Samsen P., Polinsky R.J., Masco W., da Silva H.A.R., Haines J.L., Parica-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;

RA "Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease.";

RT Nature 375:754-760(1995).

RL [2]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=129/SV;

RX MEDLINE=97442406; PubMed=9295283;

RA Mitsuda N., Roses A.D., Vittek M.P.;

RT "Transcriptional regulation of the mouse presentin1 gene.";

RL J. Biol. Chem. 272:23489-23497(1997).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=SAM P8; TISSUE=Hippocampus;

RA Kumar V.B., Vyase K.C., Choudhary V., Franko M., Flood J.F., Morley J.E.;

RT "Molecular cloning and tissue distribution of presentin-1 in senescence accelerated mice (SAM P8) mice.";

RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=FVB/N; TISSUE=Eye, Liver, and Retina;

RX MEDLINE=22388257; PubMed=12477932;

RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buscaw K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heich F., Datschenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stadelstein M., Soares M.B., Bonalant T.L., Schaefer T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosnak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez Y., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RP INTERACTION WITH DOCK3.

RC TISSUE=Brain;

RX MEDLINE=20312861; PubMed=10854253;

RA Kashiva A., Yoshida H., Lee S., Paladino T., Liu Y., Chen O., Dargusch R., Schubert D., Kimura H.;

RT "Isolation and characterization of novel presentin binding protein.";

RL J. Neurochem. 75:109-116(2000).

CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase complex, an endoprotease complex that catalyzes the intramembrane

CC cleavage of integral membrane proteins such as Notch receptors and App (beta-amyloid precursor protein). Requires the other members of the gamma-secretase complex to have a protease activity. May play a role in intracellular signaling and gene expression or in linking chromatin to the nuclear membrane. Regulates epithelial-cadherin function (By similarity).

CC SUBUNIT: Homodimer. Component of the gamma-secretase complex, a complex composed of a presentin homodimer (PSN1 or PSEN1) and nicastrin (NCSTN), Aph1 (APH1 or Aph1b) and Pen2. Such minimal complex is sufficient for secretase activity, although other components may exist. Predominantly heterodimer of a N-terminal (NTP) and a C-terminal (CTP) endoproteolytical fragment. Associates with proteolytic processed C-terminal fragments C93 and C99 of the amyloid precursor protein (APP). Associates with Notch1. Binds to cadherin 1, beta-catenin, delta-2 catenin and plakophilin 4. Interacts with Dock3. Interacts with HHR23D, FLNA and FLNB (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and endoplasmic reticulum (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=P49763-1; Sequence=Displayed;

CC Name=2;

CC IsoId=P49763-2; Sequence=VSP_008381, VSP_008382;

CC Note=Due to inframe retention. No experimental confirmation available;

CC -1- PTM: Phosphorylated on serine residues (By similarity).

CC -1- SIMILARITY: Belongs to the presentin family.

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CC -----

CC EMBL, I42177; AAC2094.1; -

CC EMBL, AF007560; AAB72049.1; -

CC EMBL, AF149111; AAF73153.1; -

CC EMBL, BC014744; AAH14744.1; -

CC EMBL, BC030409; AAH30409.1; -

CC PIR, I78388; I78388.

CC MEROPS, A22.001; -

CC MGD; MG1:1202717; Psen1.

CC GO; GO:0005783; C:Endoplasmic reticulum; IDA.

CC GO; GO:0016020; C:membrane; IDA.

CC GO; GO:0005515; F:protein binding; IPI.

CC InterPro: IPR006639; Peptidase_A22.

CC InterPro: IPR001108; Peptidase_A22A.

CC Pfam: PF01080; Presentin; 1.

CC PRINTS; PRO1072; PRESENTIN.

CC Transmembrane; Phosphorylation; Endoplasmic reticulum; Golgi stack; KX Alternative splicing.

CC CHAIN 1 298 PRESENTIN 1 NTP SUBUNIT (BY SIMILARITY).

CC CHAIN 299 467 PRESENTIN 1 CTP SUBUNIT (BY SIMILARITY).

CC DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 83 103 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 104 132 LUMENAL (POTENTIAL).

CC TRANSMEM 133 153 POTENTIAL.

CC DOMAIN 154 160 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 161 181 POTENTIAL.

CC DOMAIN 182 194 LUMENAL (POTENTIAL).

CC TRANSMEM 195 215 POTENTIAL.

CC DOMAIN 216 220 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 221 241 POTENTIAL.

CC DOMAIN 242 244 LUMENAL (POTENTIAL).

CC TRANSMEM 244 264 POTENTIAL.

CC DOMAIN 265 407 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 408 428 POTENTIAL.

CC TRANSMEM 433 453 POTENTIAL.

FT	SITE	291	232	ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).
FT	SITE	292	293	ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY SIMILARITY).
FT	VARSPLIC	257	261	DIVAV -> GKAQD (in isoform 2).
FT	VARSPLIC	262	467	/Ffid=VSP_008381. Missing (in isoform 2).
FT	VARIANT	9	9	/Ffid=VSP_008382. S -> T (IN STRAIN SAM P8).
FT	VARIANT	40	40	D -> E (IN STRAIN SAM P8).
FT	VARIANT	67	67	E -> CM (IN STRAIN SAM P8).
FT	VARIANT	196	196	V -> L (IN STRAIN SAM P8).
FT	VARIANT	321	322	ER -> RED (IN STRAIN SAM P8).
SO	SEQUENCE	467 AA;	52639 MW;	D07215B4BD20549 CRC64;
Query Match	Best Local Similarity	93.2%;	Score 2228;	DB 1; Length 467;
Matches	433;	Conservative	19;	Mismatches 17; Indels 0; Gaps 0
QY	1	MTLPLPPLSYFQNAQKSEDNHLSNTVRQNDNRKREQENDRSLGHPEPISNRPQGNR	60	
Db	1	MTLPLPPLSYFQNAQKSEDNHLSNTVRQNDNRKREQENDRSLGHPEPISNRPQGNR	60	
QY	61	QVVEQDEEDEDLTLKYGAKHYIMFVPTLCMVVATIKSVFTRKQGLIYPTFE	120	
Db	61	QVVEQDEEDEDLTLKYGAKHYIMFVPTLCMVVATIKSVFTRKQGLIYPTFE	120	
QY	121	DTEVQGRALHSLTNAALMISIVYVMTLLVLYKRCYKTHAWLIISSLLIFFPSFI	180	
Db	121	DTEVQGRALHSLTNAALMISIVYVMTLLVLYKRCYKTHAWLIISSLLIFFPSFI	180	
QY	181	YLGEVFQTVNAVADYITVALILMNEGVGMKSIHMKGPLRLQQAYLIMISALMAVFIKX	240	
Db	181	YLGEVFQTVNAVADYITVALILMNEGVGMKSIHMKGPLRLQQAYLIMISALMAVFIKX	240	
QY	241	LPPEMTALIAVSVYDVYVAVCLIKGPLRMVYETQENETLFPALISSTMTVLNMAE	300	
Db	241	LPPEMTALIAVSVYDVYVAVCLIKGPLRMVYETQENETLFPALISSTMTVLNMAE	300	
QY	301	GDEPAQRRVSKNSKNAESTERESODTVAENDDGFSEMEQORDSHLGHSTPESRAA	360	
Db	301	GDEPAQRRVSKNSKNAESTERESODTVAENDDGFSEMEQORDSHLGHSTPESRAA	360	
QY	361	VOEISSISLAGEPBERGVKLGIGPFIYSVYVGSASTAGSDMTIACVAILIGLCL	420	
Db	361	VOEISSISLAGEPBERGVKLGIGPFIYSVYVGSASTAGSDMTIACVAILIGLCL	420	
QY	421	TLTLALFFKALPALPDISITFGVLVEFYATDYLQPFMDQLAFHOFYI	467	
Db	421	TLTLALFFKALPALPDISITFGVLVEFYATDYLQPFMDQLAFHOFYI	467	
RESULT 5	PSN1 RAT	STANDARD;	PRT;	468 AA.
AC	P9787;	P97529;		
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	15-MAR-2004	(Rel. 43, Last annotation update)		
DE	Presentin 1	(PS-1) (s182 protein).		
GN	PSN1	OR PSN1.		
OS	Rattus norvegicus	(Rat).		
OC	Eukaryota; Metazoa; Chordata; Scintate; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Brain;			
RA	MEDLINE=97199371; PubMed=9047347;			
RA	Taniguchi T, Hashimoto T, Taniguchi R, Shimada K, Yamada T, Yaeuda M, Nakai M, Terashima A, Koizumi T, Maeda K, Tanaka C, RT			
RT	"Cloning of the CDNA encoding rat Presentin-1."			
Gene	186;73-75(1997).			

RN	[2]	SEQUENCE FROM N.A.
RP		STRAIN-Mistat; TISSUE=Brain;
RC		MEDLINE=96255262; PubMed=8710164;
EX		Takahashi H., Murayama M., Takashima A., Mercken M., Nakazato Y.,
FA		Noguchi K., Imanori K.;
RT		"Molecular cloning and expression of the rat homologue of
RL		presenilin-1.";
CC		Neurosci. Lett. 206:113-116(1996).
CC	-I-	FUNCTION: Probable catalytic subunit of the gamma-secretase
CC		complex, an endoprotease complex that catalyzes the intramembrane
CC		cleavage of integral membrane proteins such as Notch receptors and
CC		Apo beta-amyloid precursor protein). Requires the other members
CC		of the gamma-secretase complex to have a protease activity. May
CC		play a role in intracellular signaling and gene expression or in
CC		linking chromatin to the nuclear membrane. Regulates epithelial-
CC		cadherin function (By similarity).
CC	-I-	SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
CC		complex composed of a presenilin homodimer (PSEN1 or PSEN2),
CC		nicastrin (NCSTN), Aph1 (APH1A or APH1B) and PEN2. Such minimal
CC		complex is sufficient for secretase activity, although other
CC		components may exist. Predominantly heterodimer of a N-terminal
CC		(NTF) and a C-terminal (CTF) endoproteolytical fragment.
CC		Associates with proteolytic processed C-terminal fragments C83 and
CC		C99 of the amyloid precursor protein (APP). Associates with
CC		NOTCH1. Binds to cadherin 1, beta-catenin, delta-2 catenin and
CC		plakophilin 4. Interacts with DCKX3. Interacts with HERPUD1, FLNA
CC		and FBN3 (By similarity).
CC	-I-	SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
CC		endoplasmic reticulum (By similarity). (By similarity).
CC	-I-	FTM: Phosphorylated on serine residues. (By similarity).
CC	-I-	SIMILARITY: Belongs to the presenilin family.
CC		-----
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CC		or send an email to license@isb-sib.ch).
CC		-----
DR	EMBL; D82578; BAAL1575.1; -;	
DR	EMBL; D82363; BAAL1564.1; -;	
DR	MEROPS; A22.001; -;	
DR	InterPro; IPR006639; Peptidase_A22.	
DR	InterPro; IPR001108; peptidase_A22A.	
DR	Pfam; PF01080; Presenilin_1.	
DR	PRINTS; PR01072; PRESENILIN.	
KW	SMART; SMO0730; PSN; 1.	
KW	Transmembrane; Posn; 1.	
FT	CHAIN	1 298 PRESENILIN 1 GTF SUBUNIT (BY SIMILARITY).
FT	CHAIN	299 468 PRESENILIN 1 CTF SUBUNIT (BY SIMILARITY).
FT	DOMAIN	1 82 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	83 103 POTENTIAL.
FT	DOMAIN	104 132 LUMINAL (POTENTIAL).
FT	TRANSMEM	133 153 POTENTIAL.
FT	DOMAIN	154 160 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	161 181 POTENTIAL.
FT	DOMAIN	182 194 LUMINAL (POTENTIAL).
FT	TRANSMEM	195 215 POTENTIAL.
FT	DOMAIN	216 220 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	221 241 POTENTIAL.
FT	DOMAIN	242 243 LUMINAL (POTENTIAL).
FT	TRANSMEM	244 264 POTENTIAL.
FT	DOMAIN	265 407 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	408 428 POTENTIAL.
FT	TRANSMEM	433 453 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT	SITE	291 292 SIMILARITY).
FT	SITE	292 293 ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (BY
FT	CONFLICT	234 234 A -> S (IN REF. 2).
FT	CONFLICT	381 381 K -> R (IN REF. 2).

QY 300 EGDPEAQRKYSKKNANAE-----STERESODTYAENDDGSESEMEAPORSHUG 349
 DB 301 EGDPEAQRKYSKKNANAE-----STERESODTYAENDDGSESEMEAPORSHUG 360
 QY 350 PHSSTESSRAAVALSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIA 409
 DB 361 PHSSTESSRAAVALSSSILAGEDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIA 420
 QY 410 CPVALILGLCTLLTLLAIFKKALPALPISITRGLVYFAPNDYVQFPMOALFHOPIYI 467
 DB 421 CPVALILGLCTLLTLLAIFKKALPALPISITRGLVYFAPNDYVQFPMOALFHOPIYI 478

RESULT 7
 PSN1_XENLA STANDARD; PRT; 433 AA.
 ID PSN1_XENLA STANDARD; PRT; 433 AA.
 AC 012976;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presentin alpha.
 GN PS-ALPHA.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97223465; PubMed=9070286;
 RA Tsuchimura A., Yasojima K., Hashimoto-Gotoh T.;
 RT "Cloning of Xenopus presentin-alpha and -beta cDNAs and their
 differential expression in oogenesis and embryogenesis.";
 RL Biochem. Biophys. Res. Commun. 231:392-396(1997).
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors (By
 similarity). May play a role in negative regulation of apoptotic
 cascades during oogenesis and embryogenesis, and in
 developmentally matured tissues such as brain tissue.
 CC -1- SUBUNIT: Homodimer. Probable component of the gamma-secretase
 complex, a complex composed of a presentin homodimer (PS-alpha or
 PS-beta), nicastrin (NCTN), Aph1 and PEN2 (probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highest expression in ovaries and to a lesser
 extent in testis, intestine, kidney, brain, eye and lung. Weak
 expression in liver and heart. Present in trace amounts in
 skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: Abundant in early stages of oogenesis. The
 expression is rapidly reduced between meiotic maturation and
 fertilization stages.
 CC -1- SIMILARITY: Belongs to the presentin family.
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 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

DR EMBL; D84427; BAA19570.1; -
 DR PIR; JCS390; JCS390.
 DR MEROPS; A22.001; -
 DR InterPro; IPR006639; Peptidase_A22.
 DR InterPro; IPR001108; Peptidase_A22A.
 DR Pfam; PF01080; Presentin, 1.
 DR PRINTS; PR01072; PRESENTIN.
 DR SMART; SM00730; PSN.1.
 DR Transmembrane; Glycoprotein.
 FT TRANSMEM 48 68 POTENTIAL.
 FT TRANSMEM 99 119 POTENTIAL.

FT TRANSMEM 127 147 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 184 204 POTENTIAL.
 FT TRANSMEM 210 230 POTENTIAL.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT CARBOHYD 245 245 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 433 AA; 48301 MW; 71CBE3FEB93C0AF CRC64;

Query Match 75.3%; Score 1801; DB 1; Length 433;
 Best Local Similarity 82.8%; Pred. No. 3.8e-118;
 Matches 355; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

QY 39 NDRSLGPEPLSGRPGNGRQVVEDEDEELTKYGAHYIMFVPTLCMVVVA 98
 DB 5 SERNSNSESQSGNGQSSQVLEQDEDEDELTKYGAHYIMFVPTLCMVVVA 64
 QY 99 TIKSVSFYTRKDGOLITPTEDTEVQGRALSHILNAIMTSIVYVNTILLVYKRC 158
 DB 65 TIKSVSFYTRPDGOLITPTEDTESVQGRALSHILNAIMTSIVYVNTILLVYKRC 124
 QY 159 YKVTHAMLIISLLPFESFIYGEVFKTNVAVDYITVALIMNFVGVMISIMKGP 218
 DB 125 YKVTHAMLIISLLPFESFIYGEVFKTNVAVDYITVALIMNFVGVMISIMKGP 184
 QY 219 LRLQAVLIMISALMALVFIKLPENTAMLLAVISYVDLVAVLCKGLPMVETAOER 278
 DB 185 LRLQAVLIMISALMALVFIKLPENTAMLLAVISYVDLVAVLCKGLPMVETAOER 244
 QY 279 NETLPALISSTWVIMVNAEGDEPQORRYSKSNASTERESODTYAENDDGSE 338
 DB 245 NETLPALISSTWVIMVNAEGDEPQORRYSKSNASTERESODTYAENDDGSE 304
 QY 339 EWEACRSHLGHPRSTPSRAAVALSSSILAGEDPEERGVKLGDFIFYSVLVGRASA 398
 DB 305 EWEACRSHLGHPRSTPSRAAVALSSSILAGEDPEERGVKLGDFIFYSVLVGRASA 364
 QY 399 TASGWNNTTICFVALILGLCTLLTLLAIFKKALPALPISITRGLVYFAPNDYVQFPMO 458
 DB 365 TASGWNNTTICFVALILGLCTLLTLLAIFKKALPALPISITRGLVYFAPNDYVQFPMO 424
 QY 459 QLAHQFYI 467
 DB 425 QLAHQFYI 433

RESULT 8
 PSN1_BRARE STANDARD; PRT; 456 AA.
 ID PSN1_BRARE STANDARD; PRT; 456 AA.
 AC 09M677;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Presentin 1 (PS1) (ZF-PS1).
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NX NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF ASP-374.
 RX MEDLINE=9452701; PubMed=10521267;
 RA Leimer U., Lun K., Romig H., Walter J., Gruenberg J., Brand M.,
 Haase C.;
 RT "Zebrafish (Danio rerio) presentin promotes aberrant amyloid
 beta-peptide production and requires a critical aspartate residue for
 its function in amyloidogenesis.";
 RL Biochemistry 38:13602-13609(1999).
 RP SEQUENCE FROM N.A.


```

RC TISSUE-Embryo;
RA Strausberg R.U.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
CC complex, an endoprotease complex that catalyzes the intramembrane
CC cleavage of integral membrane proteins such as Notch receptors (By
CC similarity).
CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
CC complex composed of a presenilin homodimer (PSEN1 or PSEN2),
CC nicastrin, APL1 and PEN2 (probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
CC endoplasmic reticulum (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC Ubiquitously expressed during embryogenesis.
CC -1- PTM: Cleaved probably due to some autocleavage.
CC -1- SIMILARITY: Belongs to the presenilin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AJ132931; CAB40386.1; -.
CC MEROPS: A22.001; AAH54639.1; ALT_INIT.
CC ZFIN: ZDB-GENE-990119-4; pscn1.
CC InterPro: IPR006639; Peptidase_A22.
CC InterPro: IPR001108; Peptidase_A22A.
CC Pfam: PF01080; Presenilin; 1.
CC PRINTS: PR01072; PRESENILIN.
CC SMART: SM00730; PSN; 1.
CC Transmembrane; Endoplasmic reticulum; Golgi stack.
CC TRANSMEM 71 91 POTENTIAL.
CC TRANSMEM 122 142 POTENTIAL.
CC TRANSMEM 155 175 POTENTIAL.
CC TRANSMEM 184 204 POTENTIAL.
CC TRANSMEM 210 230 POTENTIAL.
CC TRANSMEM 233 253 POTENTIAL.
CC TRANSMEM 337 417 POTENTIAL.
CC TRANSMEM 422 442 POTENTIAL.
CC MOTRGEN 374 374 D->A. ABOLISHES ITS ENDOPROTEOLYSIS.
CC CONFLICT 308 308 PROBABLY LOSS OF FUNCTION.
CC CONFLICT 317 317 MISSING (IN REF. 2).
CC SEQUENCE 456 AA; 50981 MW; B90C42280C874F8D CRC64;

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Query Match 67.5%; Score 1614.5; DB 1; Length 456;
 Best Local Similarity 72.1%; Pred. No. 3.8e-105; Indels 19; Gaps 7;
 Matches 334; Conservative 32; Mismatches 78; Indels 19; Gaps 7;

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QY 12 QNAQMSEDNHLSTNTRSQNDNEROEHNDRSLGHEPELSNGRPOGNSQYV-EQDEBED 70
DB 6 QNAANVNDGMDTRHRTSSTAAPSRNEVELNGP-----PTAPPPQVVTSEDED 58
QY 71 EELTKGAKHYIMFVPTLCMVVAVATIKSVSYTKDG-QILYTFETDTEVGORA 123
DB 59 EELTKGAKHYIMFVPTLCMVVAVATIKSVSYTKDQQLYTFEEDTEVGORA 118
QY 130 LHSINAAIMISVIVMTILLVLYKRCYKVIHMLIISLLIFFPSFYLYGEVEFTY 189
DB 119 LHSINAAIMISVIVMTILLVLYKRCYKVIHMLIISLLIFFPSFYLYGEVEFTY 178
QY 130 NVAADYIYVALLINFGVVGMSIHWKGPLRLOQAYLIMISALVALVITKLPETANLI 245
DB 179 NVAADYIYVALLINFGVVGMSIHWKGPLRLOQAYLIMISALVALVITKLPETANLI 238
QY 250 LAVISVYDVAVLCJKGPLMLVETAOENETLFPALISYSTMVWLVNMAEGDEAQRV 309
DB 239 LAISVYDVAVLCJKGPLMLVETAOENETLFPALISYSTMVWLVNMAEGDEAQRV 294

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QY 310 SKNSKNAESTERE---SODTYAENDDGFSEHWEKQRPDSHLCPRHSTPESRAVQELSS 366
DB 295 -NNSSHVPQOEKQVAVMAPTAQEDDGGFTPAWVHQQHQPKWSTESRRQIDEMPS 353
QY 367 S--ILGDEPEERGVKLGDFIFYSVLVGKASATAGSMNTTIACFVAILGLCTLL 424
DB 354 ARPPPADDEERGVKLGDFIFYSVLVGKASATAGSMNTTIACFVAILGLCTLL 413
QY 425 LAIFKALPALPISITFGVVFATDYLYQPFMDQAFHQFYI 467
DB 414 LAIFKALPALPISITFGVVFATDYLYQPFMDQAFHQFYI 456

RESULT 9
PSN2_XENLA STANDARD; PRT; 449 AA.
ID PSN2_XENLA
AC 012977;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Presenilin beta.
GN PS-BETA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97223465; PubMed=9070286;
RA Tsujimura A., Yasojima K., Hashimoto-Gotch T.;
RT "Cloning of Xenopus presenilin-alpha and -beta cDNAs and their
RT differential expression in oogenesis and embryogenesis.";
RT Biochem. Biophys. Res. Commun. 231:392-396 (1997).
CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
CC complex, an endoprotease complex that catalyzes the intramembrane
CC cleavage of integral membrane proteins such as Notch receptors (By
CC similarity). May play a role in negative regulation of apoptotic
CC cascades during oogenesis and embryogenesis, and in
CC developmentally matured tissues such as brain tissue.
CC -1- SUBUNIT: Homodimer. Probable component of the gamma-secretase
CC complex, a complex composed of a presenilin homodimer (PS-alpha or
CC PS-beta), nicastrin (NCSTN), APL1 and PEN2 (probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Highest expression in ovaries and to a lesser
CC extent in kidney, brain, eye and lung. Weak expression in testis,
CC intestine, liver and heart. Present in trace amounts in skeletal
CC muscle.
CC -1- DEVELOPMENTAL STAGE: Abundant in early stages of oogenesis after
CC which it is nearly constant.
CC -1- SIMILARITY: Belongs to the presenilin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, D84428; BAA19571.1; -.
CC PIR, JCS391; JCS391.
CC MEROPS: A22.002; -.
CC InterPro: IPR006639; Peptidase_A22.
CC InterPro: IPR001108; Peptidase_A22A.
CC Pfam: PF01080; Presenilin; 1.
CC PRINTS: PR01072; PRESENILIN.
CC SMART: SM00730; PSN; 1.
CC Transmembrane; Glycoprotein.
CC TRANSMEM 92 112 POTENTIAL.
CC TRANSMEM 142 162 POTENTIAL.
CC TRANSMEM 170 190 POTENTIAL.

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RL J. Neurosci. 18:914-922(1998).
 RN (10)
 RP MUTAGENESIS OF ASP-366.
 RX MEDLINE=99428546; PubMed=10497236;
 RA Steiner H., Duff K., Capell A., Romig H., Grim M.G., Lincoln S.,
 RA Hardy J., Yu X., Picciano M., Fichtelner K., Citron M., Kopan R.,
 RA Persol B., Keck S., Baader M., Tomita T., Iwatsubo T., Baumgaertel R.,
 RA Haass C.,
 RT "A loss of function mutation of presenilin-2 interferes with amyloid
 RT beta-peptide production and notch signaling.";
 RL J. Biol. Chem. 274:28669-28673(1999).
 RN (11)
 RP MUTAGENESIS OF ASP-263 AND ASP-366.
 RX MEDLINE=20119269; PubMed=106552302;
 RA Kimberly W.T., Xia W., Rahmati T., Wolfe M.S., Selkoe D.J.,
 RT "The transmembrane aspartates in presenilin 1 and 2 are obligatory for
 RT gamma-secretase activity and amyloid beta-protein generation.";
 RL J. Biol. Chem. 275:3173-3178(2000).
 RN (12)
 RP INTERACTION WITH HERPUD1.
 RX MEDLINE=2193537; PubMed=11799129;
 RA Sai X., Kawamura Y., Kokame K., Yamaguchi H., Shirashi H., Suzuki R.,
 RA Suzuki T., Kawachi M., Miyata T., Kitamura T., De Strooper B.,
 RA Yanagisawa K., Komano H.,
 RT "Endoplasmic reticulum stress-inducible protein, Herp, enhances
 RT presenilin-mediated generation of amyloid beta-protein.";
 RL J. Biol. Chem. 277:12915-12920(2002).
 RN (13)
 RP REVIEW ON VARIANTS.
 RX MEDLINE=98180715; PubMed=9521418;
 RA Cruts M., van Broeckhoven C.,
 RT "Presenilin mutations in Alzheimer's disease.";
 RL Hum. Mutat. 11:183-190(1998).
 RN (14)
 RP VARIANT AD HIS-62.
 RX MEDLINE=98046005; PubMed=9384602;
 RA Cruts M., van Duijn C.M., Backovens H., van den Broeck M.,
 RA Wehrli A., Smeets S., Sherrington R., Hutton M., Hardy J.,
 RA St George-Hyslop P.H., Hofman A., van Broeckhoven C.,
 RT "Estimation of the genetic contribution of presenilin-1 and -2
 RT mutations in a population-based study of presenile Alzheimer
 RT disease.";
 RL Hum. Mol. Genet. 7:43-51(1998).
 RN (15)
 RP VARIANT AD ILE-148.
 RA Lao J.I., Beyer K., Fernandez-Novoa L., Cacabelos R.,
 RT "A novel mutation in the predicted TM2 domain of the presenilin 2 gene
 RT in Spanish patient with late-onset Alzheimer's disease.";
 RL Neurogenetics 1:293-296(1998).
 RN (16)
 RP VARIANTS AD PRO-122 AND ILE-239.
 RX MEDLINE=20100613; PubMed=10631141;
 RA Finch U., Mueller-Thomsen T., Mann U., Eggers C., Marksteiner J.,
 RA Meins W., Biret G., Alberici A., Hock C., Nitsch R.M., Gal A.,
 RT "High prevalence of pathogenic mutations in patients with early-onset
 RT dementia detected by sequence analyses of four different genes.";
 RL Am. J. Hum. Genet. 66:110-117(2000).
 RN (17)
 RP FUNCTION: Probable catalytic subunit of the gamma-secretase
 CC complex, an endoprotease complex that catalyzes the intramembrane
 CC cleavage of integral membrane proteins such as Notch receptors and
 CC APP (beta-amyloid precursor protein). Requires the other members
 CC of the gamma-secretase complex to have a protease activity. May
 CC play a role in intracellular signaling and gene expression or in
 CC linking chromatin to the nuclear membrane. May function in the
 CC cytoplasmic partitioning of proteins.
 CC SUBUNIT: Interacts with DOK3 (By similarity). Homodimer.
 CC Component of the gamma-secretase complex, a complex composed of a
 CC presenilin homodimer (PSEN1 or PSEN2), nicastrin (NCSTN), APH1
 CC (APH1A or APH1B) and PEN2. Such minimal complex is sufficient for
 CC secretase activity, although other components may exist. Interacts
 CC with HERPUD1, FLN4 and FLN5.
 CC SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 CC endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49810-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49810-2; Sequence=VSP_005194;
 CC -1- TISSUE SPECIFICITY: Isoform 1 is seen in the placenta, skeletal
 CC muscle and heart while isoform 2 is seen in the heart, brain,
 CC placenta, liver, skeletal muscle and kidney.
 CC -1- PIM: Heterogeneous proteolytic processing generates N-terminal and
 CC C-terminal fragments.
 CC -1- PTM: Phosphorylated on serine residues.
 CC -1- DISEASE: Defects in PSEN2 are a cause of early-onset Alzheimer
 CC disease (AD) [MIM:104300]; which is the most severe form of the
 CC disease, with complete penetrance and an onset occurring as early
 CC as 30 years of age. The second form is late-onset AD (LOAD), with
 CC mean age of onset greater than 58 years. AD is an autosomal
 CC dominant neurodegenerative disorder characterized by progressive
 CC dementia, parkinsonism, and deposition of fibrillar amyloid
 CC proteins as intraneuronal neurofibrillary tangles, extracellular
 CC amyloid plaques and vascular amyloid deposits.
 CC -1- DISEASE: Three causative genes have been identified that when
 CC mutated lead to presenile Alzheimer's disease: APP (amyloid
 CC precursor protein gene), PSEN1 and PSEN2. These three genes
 CC account for half of the families with autosomal dominant presenile
 CC AD, which represent approximately 10% of the whole AD population.
 CC In addition, apolipoprotein E has been identified as a risk-
 CC modifying locus.
 CC -1- SIMILARITY: Belongs to the presenilin family.
 CC -1- DATABASE: NAME=Alzheimer Research Forum;

Query Match 60.7%; Score 1452; DB 1; Length 448;
 Best Local Similarity 65.2%; Pred. No. 7,4e-94;
 Matches 304; Conservative 40; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELPAFLSYFQNAQMSNDNHSNTVRSQNDNRREGEHNDNR-SIGHPEPLSNGRQGSRRQ 61
 DB 24 EEPFRCCQGRQPEEGENTPAQRSENEDEGDEPDRVYCGVP-----GRPG----- 74
 QY 62 VVEDEDEDEDELTKYAKAKVIMLFVPTLCMVVVAATIKSVFYTRKQQLIYPTPTD 121
 DB 75 -----LEBELTKYAKAKVIMLFVPTLCMVVVAATIKSVFYTRKQQLIYPTPTD 127
 QY 122 TETVGPALSHSINAAIMISYIVYMTLLVLYIKRYKYTHAMLLISLLFFSPFIY 181
 DB 128 TPVSGQRILNSVNTLLIMISIVYMTLLVLYIKRYKYTHAMLLISLLFFFYIY 187
 QY 182 LGEVFKTYNAVADYITVALIIMFGVVGMSIHMKGPLRQCAVLLIMISALMLVPIKYL 241
 DB 188 LGEVLTQYNAVAMQPTLLVYVMPFGAVGWCCHMKGPLVQCAVLLIMISALMLVPIKYL 247
 QY 242 PENTAMTILAVISYDVAIVAVLCKGPIRMVETPAQENETLFPALITSSMTMVLVNAAG 301
 DB 248 PEMSAWVILGASIVYDVAIVAVLCPGPIRMVETPAQENETLFPALITSSMTMVLVNAAG 307
 QY 302 DPENQRYSKSKNAESTERESQDTVAENDDGFSSEMEACRDSHLCGRSTPESRAV 361
 DB 308 DPSSQGL--QLRPDP--MEEDSYDSRG--PSYVFPFPLTGYG----- 349
 QY 362 QELSSILAGDPPEERGVKLGDFITYSVLVGAASATAGDMNTTACRYALLIGCLT 421
 DB 350 EEL-----EESEERGVKLGDFITYSVLVGAASATAGDMNTTACRYALLIGCLT 402
 QY 422 LLALAFKKALPALPISITRGLVVPFADYLVQPFQMLAFHOFYI 467
 DB 403 LLALAFKKALPALPISITRGLVVPFADYLVQPFQMLAFHOFYI 448

RESULT 11
 PSEN2_MTCMU STANDARD; PRT; 445 AA.
 ID_PSEN2_MTCMU
 AC P73801;
 DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presentin 2 (PS-2) (Fragment).
 GN PSN2 OR PSN12 OR PS2.
 OS Microtus murinus (Lesser mouse Lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Cheirogaleidae;
 OC Microtus.
 NC NCBI_TaxID=30608;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99167105; PubMed=10069575;
 RA Calenda A., Mestre-Frances N., Czech C., Pradier L., Peller A.,
 RA Perret M., Bons N., Bellis M.,
 RT "Cloning of the presentin 2 cDNA and its distribution in brain of
 the primate, Microtus murinus: coexpression with betaAPP and Tau
 proteins." Dis. 5:323-333(1998).
 RL Neurobiol.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. May function in the
 cytoplasmic partitioning of proteins (By similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 complex composed of a presentin homodimer (PSN1 or PSN2),
 nicastrin (NCSTN), Aph1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Interacts with DOK3. Interacts with
 HERPUD1, FLNA and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and
 endoplasmic reticulum (By similarity).
 CC -1- PM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Belongs to the presentin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as the content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, Y10140, CAA71228.1, -.
 DR MEROPS; A22.002, -.
 DR InterPro; IPR006639, Peptidase_A22.
 DR InterPro; IPR001108, Peptidase_A22A.
 DR Pfam; PF01080, Presentin; 1.
 DR PRINTS; PRO1072, PRESENTIN.
 DR SMART; SM00730; PSN. 1.
 KM Transmembrane1; Phosphorylation; Endoplasmic reticulum; Golgi stack;
 FT CHAIN 1 297 PRESENTIN 2 NTF SUBUNIT (BY SIMILARITY).
 FT 298 445 PRESENTIN 2 CTF SUBUNIT (BY SIMILARITY).
 FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 88 108 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 109 138 LUMENAL (POTENTIAL).
 FT DOMAIN 139 159 POTENTIAL.
 FT DOMAIN 160 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 187 POTENTIAL.
 FT TRANSMEM 188 200 LUMENAL (POTENTIAL).
 FT DOMAIN 201 221 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 222 223 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 224 244 LUMENAL (POTENTIAL).
 FT TRANSMEM 245 271 POTENTIAL.
 FT DOMAIN 272 368 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 369 409 POTENTIAL.
 FT TRANSMEM 414 434 POTENTIAL.
 FT NON_TER 445
 SQ SEQUENCE 445 AA; 49475 MW; 0A01A764659E052 CRC64;

Query Match 60.2%; Score 1440; DB 1; Length 445;
 Best Local Similarity 65.0%; Pred. No. 5e-93;
 Matches 301; Conservative 42; Mismatches 78; Indels 42; Gaps 8;
 QY 3 ELIAPLSTFYQNAQMSDNHLSNTRPSQDNREORSHNDR-SLGHPEPLSGRQGSRSQ 61
 DB 24 ESPSPRSQCOEGQGEDDSTAOWRIQDEEDGEDDPRVYSSGP-----GRPG----- 74
 QY 62 VVEQDEEDDELLTKYGAHYIMLFVPTLGMVVAVATIKSVSPYTRKQGLIYPTED 121
 DB 75 -----PEEELTKYGAHYIMLSVPTLGMVVAVATIKSVRYTEKNGOLITPTED 127
 QY 122 TETVGORALHSILNAINWISYVWTILVLYKRCRYTHANLILSSLLLPFSPY 181
 DB 128 TPVSQRLNSVLMNLMISVIVMTIFLVLYKRCYKPLHGWLMSSLMFLFYIY 187
 QY 162 LGEVFKYNAVVDYITVTLALINFGVGMISIHMKGPLRQAYLIMISALMALVFTKY 241
 DB 168 LGEVKTIVNAMDPTVLVTWNNGAVGMCIHMKGPLMQAYLILASALMALVFTKY 247
 QY 242 PEWTAMLLAVISYVDLVAVLCLKGPLMVLVETAQERNETLFPALISSTWVLVNAEG 301
 DB 248 PEWSAVILGAIISYDILVAVLCPKGPLMLVETAQERNETLFPALISASAVWTVGAKL 307
 QY 302 DPEAGRYSKSKNAESTERESQTVANENDGSGPSEMEQRDSHGPHSTESRAV 361
 DB 308 DSSSQAL--QLPYDP--MEEDSYSLGE---PSIPEVFAPLPGYP----- 349
 QY 362 CELSSILAGEDPERGVKLGIDPIFYSLVVGKASATASGDWNTTACFAVILIGLCT 421
 DB 350 EEL-----EEERGVKLGIDPIFYSLVVGKAAATSGDWMNTTACFAVILIGLCT 402
 QY 422 LLLLVFKKALPALPISITFGVTFPARDIYVOPMDLAHQ 464
 DB 403 LLLLVFKKALPALPISITFGVTFPARDIYVOPMDLAHQ 445
 RESULT 12
 ID PSN2_BOVIN STANDARD. PRT; 449 AA.
 AC Q9X796;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Presentin 2 (PS-2).
 GN PSN2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Sahana N., Shitaraawa T., Mori H.,
 RT "Molecular cloning of bovine presentin 2 gene."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Probable catalytic subunit of the gamma-secretase
 complex, an endoprotease complex that catalyzes the intramembrane
 cleavage of integral membrane proteins such as Notch receptors and
 APP (beta-amyloid precursor protein). Requires the other members
 of the gamma-secretase complex to have a protease activity. May
 play a role in intracellular signaling and gene expression or in
 linking chromatin to the nuclear membrane. May function in the
 cytoplasmic partitioning of proteins (By similarity).
 CC -1- SUBUNIT: Homodimer. Component of the gamma-secretase complex, a
 complex composed of a presentin homodimer (PSN1 or PSN2),
 nicastrin (NCSTN), Aph1 (APH1A or APH1B) and PEN2. Such minimal
 complex is sufficient for secretase activity, although other
 components may exist. Interacts with DOK3. Interacts with
 HERPUD1, FLNA and FLNB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Golgi and

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 16:53:51 ; Search time 45 Seconds

(without alignments)
3274.378 Million cell updates/sec

Title: US-09-785-474A-30

Sequence: 1 MTELPAPLPLFYFQNAQSEDN.....ATDYLVPFMDLAFHQFYI 467

Scoring table: BLOSUM62

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1975.5	82.6	468	13 Q90X08	Q90X08 gallus galli
2	1529.5	64.0	384	13 Q73869	Q73869 cyprinus ca
3	1368	57.2	504	13 Q8W558	Q8W558 branchiosteo
4	1361.5	56.9	451	13 Q90X07	Q90X07 gallus galli
5	1360.5	56.9	525	5 Q8W559	Q8W559 branchiosteo
6	1240.5	51.9	582	5 Q9GU38	Q9GU38 helix lucor
7	675	28.2	133	6 Q8WZ65	Q8WZ65 oryctolagus
8	671	28.1	133	6 Q8WZ65	Q8WZ65 camelus dro
9	552	23.1	478	10 Q8SD32	Q8SD32 oryza sativ
10	159	6.6	291	17 Q8EX12	Q8EX12 pyrobaculum
11	132.5	5.5	455	16 Q97FJ2	Q97FJ2 clostridium
12	120.5	5.0	661	11 Q8OTG2	Q8OTG2 mus musculu
13	120.5	5.0	691	4 Q9HNS3	Q9HNS3 homo sapien
14	120	5.0	616	5 Q861Z6	Q861Z6 dictyosteli
15	118.5	5.0	309	16 Q98Q85	Q98Q85 mycoplasma
16	118	4.9	555	2 Q84DU8	Q84DU8 caudobacter

17	116.5	4.9	438	16 Q8A257	Q8A257 bacteroides
18	115.5	4.8	606	13 Q7TOP3	Q7TOP3 xenopus lae
19	115	4.8	364	16 Q92U24	Q92U24 rhizobium m
20	115	4.8	417	16 Q8RH68	Q8RH68 fusobacteri
21	115	4.8	601	5 Q95YF4	Q95YF4 drosophila
22	114.5	4.8	754	13 Q8AYP0	Q8AYP0 anguilla ja
23	113	4.7	224	2 Q8VSK2	Q8VSK2 staphylococ
24	113	4.7	539	16 Q82TG1	Q82TG1 nitrosomona
25	112	4.7	321	11 Q7TQ99	Q7TQ99 mus musculu
26	112	4.7	410	2 Q939W3	Q939W3 aeromonas s
27	111.5	4.7	339	17 Q58554	Q58554 pyrococcus
28	111	4.6	578	2 Q9RMN0	Q9RMN0 caulobacter
29	110	4.6	318	17 Q9HQ23	Q9HQ23 halobacteri
30	110	4.6	540	5 Q9VDV9	Q9VDV9 drosophila
31	110	4.6	705	11 Q8VH13	Q8VH13 rattus norv
32	110	4.6	707	10 Q9T050	Q9T050 arabidopsis
33	110	4.6	835	4 Q9ULF5	Q9ULF5 homo sapien
34	109.5	4.6	379	2 Q8KN62	Q8KN62 pseudomonas
35	109.5	4.6	408	13 Q8JG70	Q8JG70 brachydanio
36	109.5	4.6	598	10 Q82747	Q82747 arabidopsis
37	109.5	4.6	838	16 Q8DC40	Q8DC40 vibrio vuln
38	109	4.6	599	5 Q22089	Q22089 caenorhabdi
39	108	4.5	3374	12 Q8JUZ3	Q8JUZ3 montana myo
40	107.5	4.5	590	6 Q8HY49	Q8HY49 canis famli
41	107.5	4.5	699	10 Q93ZQ5	Q93ZQ5 arabidopsis
42	107	4.5	813	5 Q86HP1	Q86HP1 dictyosteli
43	106.5	4.5	571	13 Q8Q3E8	Q8Q3E8 brachydanio
44	106	4.4	269	2 Q9WYX0	Q9WYX0 pedicoccus
45	106	4.4	515	16 Q8CXCS	Q8CXCS oceanobacil

ALIGNMENTS

RESULT 1

ID	Q90X08	PRELIMINARY	PRT	468 AA.
AC	Q90X08			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Presentin 1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_Taxid=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=EL4; TISSUE=Brain;			
RA	Korade Mirnics Z., Keryanov S., Lovelock J., Corey S.J.;			
RT	"Cloning of chicken presentinins."			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY043492; AX95408.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR006639; Peptidase_A22.			
DR	Pfam; PF01080; Presentin_1.			
DR	PRINTS; PRO1072; PRESENTIN.			
DR	SMART; SM00730; PSN. 1.			
SQ	SEQUENCE 468 AA; 52812 MW; B746BDA3BAC0BPA CRC64;			

Query Match 82.6%; Score 1975.5; DB 13; Length 468;
Best Local Similarity 83.1%; Pred. No. 5.2e-156;
Matches 392; Conservative 30; Mismatches 41; Indels 9; Gaps 3;

Oy	1 MTELPAPLPLFYFQNAQSE---DNHLSNTVRSQNDNRERQSH--NDRSLGHPPLSNGRP 55
Db	1 MTELSALHPQFQHQGMENFPDNLST-----NDNSRRRNDNSERRRNDNPSGETNGP 56
Oy	56 QGNSRQVEQDEDEDELTTKYGAQAYIMLPVYTLQMTVVATLISVSYYTRKQGLLY 115

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Db      57  QNNICQVVDODEDEDELLTKYGAHVIMLFPVPLICMVVAVATISVSFYTRKQOLY 116
QY      116  TPTEDEETVGORALSHIINAAIMISYIVVNTILLVLYKRCYKVIHAMIILSSLLLF 175
Db      117  TPEEBEDDTICORALNINSLNAAIMISYIVVNTILLVLYKRCYKVIHAMIILSSLLLF 176
QY      176  FFSFIYGEVKTNNVAVDYTTVALLIMNFGVGMISIMHKGPIRLQOAVLIMISALML 235
Db      177  FFSFIYGEVKTNNVAVDYTTVALLIMNFGVGMISIMHKGPIRLQOAVLIMISALML 236
QY      236  VFIKLPMTMLIAVSVYDLVAVLCLKGLPMVETAOERNTLFPALISSTVWL 235
Db      237  VFIKLPMTMLIAVSVYDLVAVLCLKGLPMVETAOERNTLFPALISSTVWL 236
QY      236  VNMAEGDEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLEPRHSTP 355
Db      237  VNMAEGDEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSHLEPRHSTP 356
QY      356  ESRAVVOELSSILLAGEPBERGVGLGDFIFYSVLVSKASATASGDMNTTIACFVAL 415
Db      357  ESRAVVOELSSILLAGEPBERGVGLGDFIFYSVLVSKASATASGDMNTTIACFVAL 416
QY      416  IGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOFYI 467
Db      417  IGLCTLLLLAIFKKALPALPISITFGLVFFATDYLVPFMDQLAFHOFYI 468

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RESULT 2

```

ID 073869 PRELIMINARY; PRT; 384 AA.
AC 073869;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE PS1 protein (Fragment).
GN PS1.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337349; PubMed=9674592;
RA Archer S., Hirano J., Dies J.K.J., Fraser S.P., Djamez M.B.A.;
RT "Expression and localization in the fish retina of a homologue of the
RT Alzheimer's related psi gene."
RT Neuroreport 9:2049-2056 (1998).
RL EMBL: Y17128; CAA/6641.1; -.
DR MEROPS; A22.001; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR006639; Peptidase A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PF01080; Presentin_1.
DR PRINTS; PR01072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR NON TER 1
FT VARIANT 5 I -> V.
FT VARIANT 56 A -> S.
FT VARIANT 56 A -> V.
FT VARIANT 60 S -> G.
FT VARIANT 63 V -> L.
FT VARIANT 83 G -> A.
FT VARIANT 83 G -> S.
FT VARIANT 118 A -> S.
FT VARIANT 200 P -> T.
SQ SEQUENCE 384 AA; 43276 MW; F97EBFE24B31FDAA CRC64;

```

Query March 64.0%; Score 1529.5; DB 13; Length 384;
 Best Local Similarity 79.5%; Pred. No. 5.6e-119;
 Matches 311; Conservative 27; Mismatches 40; Indels 13; Gaps 6;
 QY 83 IMFLPVTLICMVVAVATISVSFYTRKDG-QLITPTEDEETVGORALSHIINAAIMIS 141

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Db      1  IMFLPVTLICMVVAVATISVSFYTRKDGQOLITPTEDEETVGORALSHIINAAIMIS 60
QY      142  VIVVNTILLVLYKRCYKVIHAMIILSSLLFFPSFIYGEVKTNNVAVDYTTVAL 201
Db      61  VIVVNTILLVLYKRCYKVIHAMIILSSLLFFPSFIYGEVKTNNVAVDYTTVAL 120
QY      202  IMNFGVGMISIMHKGPIRLQOAVLIMISALMALVFIKLPMTMLIAVSVYDLVAV 261
Db      121  IMNFGVGMISIMHKGPIRLQOAVLIMISALMALVFIKLPMTMLIAVSVYDLVAV 180
QY      262  LCLKGLPMVETAOERNTLFPALISSTVWLVNMAEGDEAQRVSKNSKNAESTE 321
Db      181  LCLKGLPMVETAOERNTLFPALISSTVWLVNMAEGDEAQRVSKNSKNAESTE 233
QY      322  RESQDTVA---ENDDGFSEWEAQRDSHLEPRHSTPESRAVVOELSSILLAG-EDPEE 376
Db      234  QENQDAVAPTAQPEDDGFTPAMVNOOCHQLGPMQSTEDSKREIQLSARPPVEDDEE 293
QY      377  RGVKGLGDFIFYSVLVSKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALP 436
Db      294  RGVKGLGDFIFYSVLVSKASATASGDMNTTIACFVALIIGLCTLLLLAIFKKALPALP 353
QY      437  ISTTGLVFFATDYLVPFMDQLAFHOFYI 467
Db      354  ISTTGLVFFATDYLVPFMDQLAFHOFYI 384

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RESULT 3

```

ID Q8WS58 PRELIMINARY; PRT; 504 AA.
AC Q8WS58;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Presentin.
GN PS.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21590369; PubMed=11733140;
RA Martinez-Mir A., Caneiro C., Gonzalez-Duarte R., Albalat R.;
RT "Characterization of the amphioxus presentin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RT Gene 279:157-164 (2001).
RL EMBL: AF369891; AAL40416.1; JOINED.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008447; HTH_LysR.
DR InterPro; IPR006639; Peptidase A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PF01080; Presentin_1.
DR PRINTS; PR01072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
SQ SEQUENCE 504 AA; 55443 MW; 9C3794D030285984 CRC64;

```

Query March 57.2%; Score 1368; DB 5; Length 504;
 Best Local Similarity 58.8%; Pred. No. 2.2e-105;
 Matches 275; Conservative 56; Mismatches 101; Indels 36; Gaps 7;
 QY 27 RSCQDNREKQANDRRSIGHPPLSNRPGQNSGVVQOEDEDEETLTKYGAHVIMLF 86
 Db 46 RSCQDNREKQANDRRSIGHPPLSNRPGQNSGVVQOEDEDEETLTKYGAHVIMLF 98
 QY 87 VPVTLICMVVAVATISVSFYTRKDGQOLITPTEDEETVGORALSHIINAAIMISVIVVM 146

```

Db 99 AVSLCMAVVAATISSITTEKNGLYITPFHEBASTASVGSISLNGALMVGILVM 158
147 TLILVLYKRCYKXV/HAMLIISLILFFSFYLYGEVFKTYNAVDYITVALLIMNG 206
159 TVFLVLYKRCYKXV/HGWLILSLMLFLFVAYIYGEVLAQVNPICYITLAIYVWNG 218
207 VVGMIISHWKGPLRLOQAVLIMISALMALVFIKYLPEMTAMILAVISYDVAVLCLKG 266
219 AVGMCIHWKGPLRLOQAVLIMISALMALVFIKYLPEMTAMILAVISYDVAVLCLKG 278
267 PLRMLVETAOERNETLFPALIIYSTVWLVNNAEDPEAKRVSXSKNAESTERES-- 324
279 PLKVLVETAOERNETLFPALIIYSTVWLVNNAEDPEAKRVSXSKNAESTERES-- 338
325 -QDTVAENDDGGFSEMEAR--DSHLGPHR-----STPERAAVQELSSILA-- 370
339 PAGAVGEEGEGFPGPNMSRQFPTRRNRCGNASDASVNSEDAKQAQNLNRSRPS 398
371 -----GDPBERGVKLGLDPIFYSVLVKASATASGDWNTTIACFVAILIGLC 419
399 GNGOQOQWEEDEDEBERGVKLGLDPIFYSVLVKAS--SNGDWNTTIACFVAILIGLC 456
420 LTLILALFKKALPALPISITGVLVFPATDVLQPPMDLAFHPYI 467
457 LTLILALFKKALPALPISITGVLVFPATDVLQPPMDLAFHPYI 504

```

RESULT 4

```

O90X07 PRELIMINARY: PRT: 451 AA.
AC O90X07:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Presentin. 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RX NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Korde Mirica Z., Kervanov S., Lovelock J., Corey S.J.
RT "Cloning of chicken presentin."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY043493; AAK95409.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PRO1080; Presentin_1.
DR PRINTS; PRO1072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
SQ SEQUENCE 451 AA; 50456 MW; 534E6364C627E8B0 CRC64;

```

Query Match 56.9%; Score 1361.5; DB 13; Length 451;
 Best Local Similarity 59.7%; Pred. No. 6.6e-105;
 Matches 283; Conservative 43; Mismatches 71; Indels 77; Gaps 7;

```

QY 3 ELPAFLSTFQNAQWSEDNHLSNTVRSQNDNRERQSHNDRSLGHEPLNSGRPOGNER-- 60
Db 25 ESPFPVSYODGLQASE-----TREACHRRKRCQ-----GSSRSP 58
QY 61 -QVAVOD-----EEDEELTKYGAKEVIMLFVPTLQMVVAVATIKSVSY 106
Db 59 NNVADEBDASDVRVRESALENEBEELTKYGAKEVIMLFVPTLQMVVAVATIKSVRFY 118
QY 107 TRKDGQLYTPPTEDTEVQRAHLSINAAIMSVIWMVILLVLYKRCYKXV/HAML 166
Db 119 TEKNQQLIYTPPSEDTPLSVGQRLINSVNTIMISVIVMTVFLVLYKRCYKXV/HGWL 178
QY 167 IISLILFFSFYLYGEVFKTYNAVDYITVALLIMNGVGMISHWKGPLRLOQAVL 226

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Db 179 ILSFMLELFTYIYLYGEVFKTYNAVDYITVALLIMNGVGMISHWKGPLRLOQAVL 238
QY 227 IMISALMALVFIKYLPEMTAMILAVISYDVAVLCLKGPLMLVETAOERNETLFPAL 286
Db 239 IMISALMALVFIKYLPEMTAMILAVISYDVAVLCLKGPLMLVETAOERNETLFPAL 298
QY 267 IYSTWVWLVNNAEGDEPEAKRVSXSKNAESTERESQDTVAENDDGGFSEMEAR 346
Db 299 IYSTWVWLVNNAEGDEPEAKRVSXSKNAESTERESQDTVAENDDGGFSEMEAR 391
QY 347 HLGPHRSTPERAAVQELSSILA-----ILAGDPEERGVKLGLDPIFYSVLVKASATA 400
Db 332 E--NHSSTSDSGIILDTREPAPSHPTLEMEBERGVKLGLDPIFYSVLVKASATA 389
QY 401 SGDWNTTIACFVAILIGLCITLILALFKKALPALPISITGVLVFPATDVLQ 454
Db 390 SGDWNTTIACFVAILIGLCITLILALFKKALPALPISITGVLVFPATDVLQ 443

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RESULT 5

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O9WS59 PRELIMINARY: PRT: 525 AA.
AC O9WS59:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Presentin.
CN PS.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomida;
OC Branchiostoma.
NCBI_TaxID=7739;
RX NCBI_TaxID=7739;
RP SEQUENCE FROM N.A.
RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.
RT "Characterization of the amphioxus presentin gene in a h-g gene-
RT density genomic region illustrates duplication during the vertebrate
RT lineage."
RL Gene 279;157-164(2001).
DR EMBL; AF369891; AAL40414.1; -.
DR EMBL; AF369890; AAL40414.1; JOINED.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LYER.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR001108; Peptidase_A22A.
DR Pfam; PRO1080; Presentin_1.
DR PRINTS; PRO1072; PRESENTIN.
DR SMART; SM00730; PSN; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
SQ SEQUENCE 525 AA; 57598 MW; 2B14CF77A80F07DE CRC64;

```

Query Match 56.9%; Score 1360.5; DB 5; Length 525;
 Best Local Similarity 56.6%; Pred. No. 9.6e-105;
 Matches 277; Conservative 56; Mismatches 99; Indels 57; Gaps 8;

```

QY 27 RQNDNRERQSHNDRSLGHEPLNSGRPOGNSRQVVEDDEBEELTKYGAKEVIMLF 86
Db 46 RSQIQIENPTDGAQDRREAG-----DGEDHGIHRH--EDDEBEELTKYGAKEVIMLF 98
QY 87 VPTLQMVVAVATIKSVSYTRKDGQLYTPPTEDTEVQRAHLSINAAIMSVIWMV 146
Db 99 AVSLCMAVVAATISSITTEKNGLYITPFHEBASTASVGSISLNGALMVGILVM 158
QY 147 TLILVLYKRCYKXV/HAMLIISLILFFSFYLYGEVFKTYNAVDYITVALLIMNG 206
Db 159 TVFLVLYKRCYKXV/HGWLILSLMLFLFVAYIYGEVLAQVNPICYITLAIYVWNG 218
QY 207 VVGMIISHWKGPLRLOQAVLIMISALMALVFIKYLPEMTAMILAVISYDVAVLCLKG 266

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Dh      219 AVGNWCIHMKGPIILLDQALIVISALMLVFIRKLPDITWTFILGALISLIDVAVLCPKG 278
Qy      267 PLRLMVELTAQERNETLFPALLIVYSTWVLVNNAEEDPEAQRVSKSKHNAE----- 319
Dh      279 PLKLVETAQERNRPFPALLIVYSTWMMFVGMADDPAAKKKKKKKKKKRADDGPOAGG 338
Qy      320 ---TEESQOT-----VAENDOGSEEWEAQR--DSHLGPR----- 352
Dh      339 FRLIDNAGSTGDADAFDSAPAGAVGEEBGFQPDNNERGHQPTRRPGRGNASDAS 398
Qy      353 -STPESRAAVOEIASSIILA-----GEPPERGVGLGIGDPIFYSVLVKASA 398
Dh      399 VNEEDARQAQNLSNRRLSPSGNQOQQQMEDEDEERGVKLGIGDPIFYSVLVKASA- 457
Qy      399 TAGSDNNTTIACVAAILIGLCTLLILAFKALPALPISITFGLVFYFATDIVVQPFMD 458
Dh      458 -SNGDNNTTIACVAAILIGLCTLLILAFKALPALPISITFGLVFYFANLVTPFTD 516
Qy      459 QLAHFQHYI 467
Dh      517 ALASQOYIV 525

```

RESULT 6					
ID	Q9GUJ8	PRELIMINARY;	PRT;	582 AA.	
DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Presentinlin.				
PS.					
OS	Helix lucorum.				
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;				
CC	Sigamurethna, Helicoidae, Helicidae, Helix.				
OX	NCBI_TaxID=31229;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Rogaev E.I., Riazanskala N.N., Dvorlanichkov G., Grigorenko A.P.,				
RT	Tyrin O.;				
RL	"Presentinlin gene isolated from mollusk Helix lucorum.";				
DR	Submitted (OCT-1999) to the EMBL/Genebank/DBD databases.				
EMBL:	AF197861; AAC26518.1;				
DR	GO; GO:0026020; C:membrane; IEA.				
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.				
DR	InferPro; IPR006639; Peptidase A22.				
DR	InferPro; IPR001108; Peptidase A22A.				
DR	Ffam; PF01080; Presentinlin. 1.				
DR	PRINTS; PRO1072; PRESENTLIN.				
DR	SMART; SMO0730; PSN: 1.				
SEQ	SEQUENCE 582 AA; 63782 MW; 07934E7C452199F0 CRC64;				
Query Match	51.9%;	Score 1240.5;	DB 5;	Length 582;	
Best Local Similarity	48.1%;	Pred. No. 1.1e-94;			
Matches 267;	Conservative 73;	Mismatches 108;	Indels 107;	Gaps 114;	
QY	9 SYFGNAQSENNHLSNTV-----RSONNRERCHENDRRSLGHPEPLS-----NGR 54				
DY	39 SRYSGLQSTEDDV-NAYFEATVVDPKQGDASSASGNNRHQVTSGAREBRAPYTE 97				
QY	55 PQGNRSROVEDDEBEDELTLTKGAKVYM-FVPTLCMNVVVAATIKSVSYTRKDGLI 114				
QY	98 PSGSN-----QDEDDDEE-TLLYGKAIVMLFIPTLLCMVVAVATISITVYTSGVYLI 151				
QY	115 YTFETEDETVGORALHSILNAAIWISVIYVMITLVVLVLYKKRCYKHAWLIISLLDL 174				
DY	152 YTFPHADVTDIGTKLMQGMANAVILLCVIVMTVVLVLLLYKKCYKRVANGWLVSSIMWL 211				
QY	175 FFFSFTIYGEVFKTNYNAVDTITVALLLWNGVGVGMISIHKGPIRLQCATLIMSALMA 234				
DY	212 FFFSFMYEQILIRANNAIPMDVTVAILIMNFGVGGLFCIIHWKGPILLQQCATYLIVSALVA 271				

```

OY      235  LVVFKTLPEMTAMLIIVASVYDLVAVCTLGPRLMIVETAOENETLPALVYSSMTMW  234
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      272  LMFIKTPMTIMAVGVWVIMDLVAVLCPGKPLMIVETQSNENIFPALLVYSSMTMW  331
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      295  LVNNAEGDPAQORVY-----KNSKFNASTERESQDTVAENDGGSEWE--AQDSH  347
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      332  FYVMADDGQSKKKQKQKXKLTGAQNSSVTPPLGKDT--DDDGGGTEHVANGTNQHS  389
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      348  LGEHRSTPESRAVQEL-----SSSIAGED-----  373
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      390  LTRAGQSQSARNAVQAFGDMVQDKRPTRNAVSHTTVYNTNSARVLATRDGAVESAVR  449
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      374  -----PERGVKLGIGPIEFVSYL  392
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      450  VNVDQDGAVVANSSQNNSTRPALQRRPLDSDSIDODSEERGVKLGIGDIFGVYL  509
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      393  VGRASATAGDWNVTIACFVALILIGLCUTLLILAIFFKALPALDISITPGVVEFATDYL  452
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      510  VGRAS--SNGDWNVTIACFVALILIGLCUTLLILAIFFKALPALDISITPGVVEFATSSL  567
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      453  VQPFMDQLAFHQFYI  467
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      568  VQPFMDLSAEQYTI  582
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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ID	QSHZ66	PRELIMINARY;	PRT;	133 AA.
AC	QSHZ66;			
DT	01-MAR-2003 (TREMBlrel. 23, Created)			
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Presentin11n-1 (Fragment).			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
CK	NCBI_Taxid=9986;			
KN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Al-Khedhary A.A., Arfin M., Al-Dukhyil A.B.;			
RT	"Molecular cloning and sequencing of the rabbit presentin11n-1 cDNA			
RT	fragment";			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY134851; AAN08498.1; "			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR006639; Peptidase_A22.			
DR	InterPro; IPR001108; Peptidase_A2A.			
DR	Pfam; PF01080; Presentin11n; 1.			
DR	SMART; SM00730; PSN; 1.			
FT	NON_TER	1	1	
FT	NON_TER	133	133	
SQ	SEQUENCE	133 AA;	15398 MW;	F79114407D741226 CRC64;
Query Match		28.2%;	Score 675;	DB 6; Length 133;
Best Local Similarity		98.5%;	Pred. NO. 2.1e-48;	
Matches 131;	Conservative	2;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	112 QLTPTFEDTETGQRAHSHILNAAIMTSIVYMTILLVLYKRCYKVIHAWLLISL	171		
DB	1 QLTPTFEDTETGQRAHSHILNAAIMTSIVYMTILLVLYKRCYKVIHAWLLISL	60		
QY	172 LLLEPFSTIYGEVFKTYNNAVDITVAALLTNGGCVGMISIHKKGPRLQOAYLIMISA	231		
DB	61 LLLEPFSTIYGEVFKTYNNAVDITVAALLTNGGCVGMISIHKKGPRLQOAYLIMISA	120		
QY	232 LMAVLEIKYLPBW 244			
DB	121 LMAVLEIKYLPBW 133			

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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:49:57 ; Search time 60 Seconds

(without alignments)
2199.161 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391

Sequence: 1 MTELPAPISYFQNAQMSEDN.....ATDYLVQFMDQIAFHOFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	99.7	467	2 AAM05751	AAM05751 Present11
2	2384	99.7	467	2 AAM27176	AAM27176 Human S18
3	2378	99.5	467	2 AAM05733	AAM05733 Present11
4	2378	99.5	467	2 AAM41430	AAM41430 PSI/467 P
5	2378	99.5	467	2 AAM23964	AAM23964 Human pre
6	2378	99.5	467	2 AAY24419	AAY24419 Human pre
7	2378	99.5	467	2 AAY23897	AAY23897 Amino aci
8	2378	99.5	467	3 AAB07971	AAB07971 Amino aci
9	2378	99.5	467	4 AAE10798	AAE10798 Human pre
10	2378	99.5	467	4 AAG63936	AAG63936 Amino aci
11	2378	99.5	467	4 AAE05466	AAE05466 Human pre
12	2378	99.5	467	5 AAE17051	AAE17051 Human mut
13	2378	99.5	467	5 AAY79916	AAY79916 Human pre
14	2378	99.5	467	5 AAO18049	AAO18049 Present11
15	2375	99.3	467	2 AAM05737	AAM05737 Present11
16	2375	99.3	467	2 AAM05755	AAM05755 Present11
17	2375	99.3	467	2 AAM05758	AAM05758 Present11
18	2374	99.3	467	2 AAM05754	AAM05754 Present11
19	2374	99.3	467	2 AAM05749	AAM05749 Present11
20	2374	99.3	467	2 AAM05747	AAM05747 Present11
21	2374	99.3	467	2 AAM05736	AAM05736 Present11
22	2374	99.3	467	2 AAM27177	AAM27177 Human mut
23	2374	99.3	467	4 AAE05563	AAE05563 Human pre
24	2373	99.2	467	2 AAM05746	AAM05746 Present11
25	2373	99.2	467	2 AAM05738	AAM05738 Present11

26	2373	99.2	467	2 AAM05748	AAM05748 Present11
27	2373	99.2	467	2 AAM05739	AAM05739 Present11
28	2373	99.2	467	2 AAM05741	AAM05741 Present11
29	2372	99.2	467	2 AAM05753	AAM05753 Present11
30	2372	99.2	467	2 AAM05740	AAM05740 Present11
31	2372	99.2	467	2 AAM05742	AAM05742 Present11
32	2372	99.2	467	2 AAM05757	AAM05757 Present11
33	2371	99.2	467	2 AAM05744	AAM05744 Present11
34	2371	99.2	467	2 AAM6770	AAM6770 Homo sapi
35	2371	99.2	467	4 AAE05564	AAE05564 Human pre
36	2370	99.1	467	2 AAM05752	AAM05752 Present11
37	2369	99.1	467	2 AAM05743	AAM05743 Present11
38	2369	99.1	467	2 AAM05745	AAM05745 Present11
39	2368	99.0	467	5 AAE17045	AAE17045 Human mut
40	2367	99.0	467	2 AAM05759	AAM05759 Present11
41	2366	99.0	467	2 AAM05750	AAM05750 Present11
42	2366	99.0	467	5 AAE17046	AAE17046 Human mut
43	2357	98.6	465	3 AAY51393	AAY51393 Human S18
44	2357	98.6	467	2 AAM1839	AAM1839 Human ear
45	2356	98.5	467	5 AAE17047	AAE17047 Human mut

ALIGNMENTS

RESULT 1
AAM05751
ID AAM05751 standard; protein; 467 AA.
XX
AC AAM05751;
XX
DT 25-MAR-2003 (revised)
DT 23-JUL-1997 (first entry)
XX
DE Present11-1 P264L mutation.
XX
XX Present11-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; muten.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 264 /label= P264L
FT XX
PN MO9634099-A2.
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96WO-CA000263.
PF
XX 28-APR-1995; 95US-00431048.
PR 28-JUN-1995; 95US-00496841.
PR 31-JUL-1995; 95US-00503359.
XX
XX (HSCR-) HSC RES & DEV LP.
XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
XX St Georgehylop PH, Fraser PE, Rommens JM;
XX WPI, 1996-497631/49.
XX
XX New present11 genes - useful for diagnosis, therapy and drug screening
XX of familial Alzheimer's disease, cerebral disorders, etc.
XX
XX Claim 3; Page; 178pp; English.
XX
CC AAM05736-W05760 represent mutated versions of the human present11-1-1
CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
CC different wild type form of present11-1 that results from alternate
CC splicing of the genomic DNA sequence. The present11s are a family of
CC highly conserved integral membrane proteins with a common structural

CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrenia, depression etc., so detection of mutations in the DNA
 CC encoding the wild type sequences can be used for diagnosis of these
 CC diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are useful
 CC as models for drug screening. The antibodies can also be used e.g. for
 CC affinity purification and in immunoassays. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX

SO Sequence 467 AA;

Query Match 99.7%; Score 2385; DB 2; Length 467;
 Best Local Similarity 99.8%; Pred. No. 2,7e-234;
 Matches 466; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNCRPOGNSR 60
 DB 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNCRPOGNSR 60
 QY 61 QVVEDEDEDEBELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYTRKQGLIYPTPE 120
 DB 61 QVVEDEDEDEBELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYTRKQGLIYPTPE 120
 QY 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 DB 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 QY 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 DB 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 QY 241 LPENTAMLLIAVISVYDLVAVLCIKGPLRLMIVTAORNETLFPALYYSSIMWLVMMAE 300
 DB 241 LPENTAMLLIAVISVYDLVAVLCIKGPLRLMIVTAORNETLFPALYYSSIMWLVMMAE 300
 QY 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 DB 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEBERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVALILIGLCL 420
 DB 361 VOELSSSIILAGEDEBERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVALILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHQFYI 467

RESULT 2

AAW27176 ID AAW27176 standard; protein; 467 AA.

XX AAW27176;

XX 09-DEC-1997 (first entry)

DE Human S182 gene, P51 locus, product related to Alzheimer's disease.

XX Mutant; antisense; antibody; vaccine; Alzheimer's disease.

OS Homo sapiens.

XX WO9708319-A1.

XX 06-MAR-1997.

XX 03-SEP-1996; 96WO-US014114.

XX 31-AUG-1995; 95US-0003054P.

PR 30-AUG-1996; 96US-00706344.
 XX (GENO) GEN HOSPITAL CORP.
 XX
 XX Tanzi RE, Maaco W;
 PI
 DR WPI; 1997-179276/16.
 DR N-PSDB; AAT85332.

PT Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants -
 PT anti-sense sequences, antibodies and vaccines to delay onset.

XX Claim 12; Page 72-73; 99p; English.

The present sequence represents the human S182 gene, PS1 locus, product.
 CC Mutant PS1 produces a gene product that increases the probability of
 CC Alzheimer's disease. A nucleic acid sequence able to hybridise to
 CC sequences coding for a mutant PS1 polypeptide can be used as probes for
 CC diagnosing an increased likelihood of contracting Alzheimer's disease.
 CC Antibodies against the mutant polypeptide can also be used for this
 CC purpose. Vectors containing or expressing a nucleic acid molecule,
 CC protein or antibody specific for mutant PS1 can be administered to a
 CC patient to reduce the likelihood, or delay the onset, of Alzheimer's
 CC disease, e.g. anti-sense RNA expression can be used to decrease
 CC expression of the PS1 peptide. Transgenic animals expressing the
 CC Alzheimer's disease protein can be used to test candidate therapeutics
 CC and to investigate the normal role of PS1. The PS1 peptide may also be
 CC included in pharmaceutical compositions (vaccines) for Alzheimer's
 CC disease therapy

SO Sequence 467 AA;

Query Match 99.7%; Score 2384; DB 2; Length 467;
 Best Local Similarity 99.8%; Pred. No. 3.4e-234;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNCRPOGNSR 60
 DB 1 MTELPALSYFQNAQMSDNHLSNTVRSQNDNRROHNDRRSLGHEPPLSNCRPOGNSR 60
 QY 61 QVVEDEDEDEBELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYTRKQGLIYPTPE 120
 DB 61 QVVEDEDEDEBELTKGAKAVIMLFVPVTLQWVVAVATIKSVSFYTRKQGLIYPTPE 120
 QY 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 DB 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 QY 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 DB 121 DTEVGGRAHLSINAAIMSVIWMTLVLVLYKRCYVTHAMLISSLLFFPSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLINFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 QY 241 LPENTAMLLIAVISVYDLVAVLCIKGPLRLMIVTAORNETLFPALYYSSIMWLVMMAE 300
 DB 241 LPENTAMLLIAVISVYDLVAVLCIKGPLRLMIVTAORNETLFPALYYSSIMWLVMMAE 300
 QY 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 DB 301 GDPAQRVRSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGHRSTPESRAA 360
 QY 361 VOELSSSIILAGEDEBERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVALILIGLCL 420
 DB 361 VOELSSSIILAGEDEBERGVKLGDFTFYSVLVKGASATASGDMNTTIACFVALILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHQFYI 467

RESULT 3

AAW05733 ID AAW05733 standard; protein; 467 AA.

XX AAM05733;
AC 25-MAR-2003 (revised)
DT 23-JUL-1997 (first entry)
XX Presentin-1-1.
XX Presentin-1; human; hps1-1; hps1-2; PS-2; integral membrane protein; AD;
XX familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
XX depression; antibody; gene expression modulator; therapy.
XX Homo sapiens.
XX MO9634099-A2.
XX 31-OCT-1996.
XX 29-APR-1996; 96WO-CA000263.
XX 28-APR-1995; 95US-00431048.
XX 28-JUN-1995; 95US-00496841.
XX 31-JUL-1995; 95US-00509359.
XX (HSCR-) HSC RES & DEV LP.
XX (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX St George's Hospital, Fraser PE, Rommens JM;
XX WPI, 1996-497631/49.
XX N-PSDB; AAV140028.
XX New presentin genes - useful for diagnosis, therapy and drug screening
XX of familial Alzheimer's disease, cerebral disorders, etc.
XX Claim 2; Page 128-130; 178pp; English.
XX AAM05733 and AAM05734 represent the two different forms of wild type
XX human presentin-1 (PS-1). The form represented by AAM05734 results from
XX alternate splicing of the genomic DNA sequence. AAM05732 represents the
XX coding sequence for wild type human PS-2. The presentins are a family of
XX highly conserved integral membrane proteins with a common structural
XX motif, common alternate splicing patterns, and common mutational hot spot
XX regions. Mutations in PS genes are implicated in familial Alzheimer's
XX disease (AD) and possibly other diseases such as cerebral haemorrhage,
XX schizophrenia, depression etc., so detection of mutations in the DNA
XX encoding these sequences can be used for diagnosis of these diseases.
XX These proteins, or vectors that express them or containing antisense
XX sequences, antibodies selective for mutant forms of these proteins (such
XX as AAM05736) and modulators of PS gene expression are potentially useful
XX for treatment of AD etc. Transgenic animals are useful as models for drug
XX screening. The antibodies can also be used e.g. for affinity purification
XX and in immunoassays. (Updated on 25-MAR-2003 to correct PI field.)
XX Sequence 467 AA;
SQ

Query Match 99.5%; Score 2378; DB 2; Length 467;
Best Local Similarity 99.6%; Pred. No. 1,46-233;
Matches. 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYQONQMSNDNLSTVRSQNDNRROSHNRSLGHPESLNRPOQNSR 60
DB 1 MTELPAPLSTYQONQMSNDNLSTVRSQNDNRROSHNRSLGHPESLNRPOQNSR 60
QY 61 QVVEQDEDEBELTLTKGAKVIMLEFVPVTLQWVVAVATIKSVSPYRKDGQIYPTFE 120
DB 61 QVVEQDEDEBELTLTKGAKVIMLEFVPVTLQWVVAVATIKSVSPYRKDGQIYPTFE 120
QY 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKVCYVIAHMLTSLILFFPSFI 180
DB 121 DTEVGGORALHSINMAIMTSIVIVMTLLVLYKYKVCYVIAHMLTSLILFFPSFI 180
QY 181 YLGEVFRTYVAVADYITVALLINFGVGMISIMHKGPELRLOQAYLIMISALMALVFITY 240

DB 181 YLGEVFRTYVAVADYITVALLINFGVGMISIMHKGPELRLOQAYLIMISALMALVFITY 240
QY 241 LPEWTAMLLIYAVSYVDLVAVLCLKGPELRMLVETAOERNTLFPALIIYSTWMLVMAE 300
DB 241 LPEWTAMLLIYAVSYVDLVAVLCLKGPELRMLVETAOERNTLFPALIIYSTWMLVMAE 300
QY 301 GDEEACRVSQKSKNAESTERESQPTVAENDCGFSEWEAORDSHLGPHRSTPSPRAA 360
DB 301 GDEEACRVSQKSKNAESTERESQPTVAENDCGFSEWEAORDSHLGPHRSTPSPRAA 360
QY 361 VOELSSSILAGDEPBERGVKLGADPIFYSLVGRKASATPSGDMNTTACFVAIILGLCL 420
DB 361 VOELSSSILAGDEPBERGVKLGADPIFYSLVGRKASATPSGDMNTTACFVAIILGLCL 420
QY 421 TLILLAIFFKALPALPISITFGLVFEYATDYLVQPMQDLAFHOFTI 467
DB 421 TLILLAIFFKALPALPISITFGLVFEYATDYLVQPMQDLAFHOFTI 467

RESULT 4
AAM41430
ID AAM41430 standard; protein; 467 AA.
XX AAM41430;
AC AAM41430;
XX 04-JUN-1998 (first entry)
XX PS1/467 protein.
XX Presentin peptide; PS1/429; immunogen; immune response; PS1 gene;
XX Alzheimer's disease; mitochondrial pathology; neurodegeneration;
XX apoptosis; PS1/467.
XX Homo sapiens.
XX MO9746678-A1.
XX 11-DEC-1997.
XX 03-JUN-1997; 97MO-US009272.
XX 06-JUN-1996; 96US-00659296.
XX 18-JUL-1996; 96US-00683315.
XX (FAR) BAYER CORP.
XX Davis UN, Chisholm JC, Drache B;
XX WPI; 1998-042186/04.
XX N-PSDB; AAV17358.
XX DNA encoding presentin peptide PS1/429 and its analogues - useful for
XX diagnosis and treatment of Alzheimer's disease.
XX Claim 7; Fig 2; 77pp; English.
XX This sequence is the PS1/467 presentin peptide. This sequence is
XX specifically stated as not being in the nucleic acid of the invention,
XX which encodes the PS1/429 presentin peptide PS1/429 (II). Cells
XX transformed with the DNA are used to produce recombinant (II) and
XX analogues, useful e.g. as immunogens for generating an immune response
XX against PS1/429. (II) is a new product of the PS1 gene, mutations in
XX which cause Alzheimer's disease (AD). The nucleic acids are generally
XX useful as probes for detection and quantification of PS1/429,
XX particularly for diagnosis of AD, especially the target sequences that
XX hybridise with probes are isolated for sequencing. Antibodies (Ab) can
XX also be diagnosed at the protein level using Ab as immunoassay reagents.
XX Ab can also be used to identify epitopes and for affinity purification of
XX peptides. Antisense nucleic acid may also be used to regulate expression
XX of the PS1/429 gene, and both nucleic acids and peptides are useful as
XX size markers in electrophoresis, chromatography etc. The transgenic
XX animals are used as models for AD, e.g. for testing drugs. Regulators of

CC the p51/429 gene or polypeptide can be used to treat e.g. AD or diseases
 CC involving mitochondrial pathology, apoptosis and neurodegeneration.
 CC Typical regulators are antisense sequences, ribozymes, aptamers,
 CC synthetic or natural compounds. (II) may also be used to target other
 CC coding sequences to particular cellular locations
 XX
 SQ Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 2; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEIPAPLSYFQNAQNSNDNHSNTVRSQNDNREKQNDHRSGLHPEPLSNRPGQNSR 60
 Db 1 MTEIPAPLSYFQNAQNSNDNHSNTVRSQNDNREKQNDHRSGLHPEPLSNRPGQNSR 60
 QY 61 QVVEQDEEDELTKKGAHVIMLPVPTLCVVAVATIKSVFTKDGQILTPFE 120
 Db 61 QVVEQDEEDELTKKGAHVIMLPVPTLCVVAVATIKSVFTKDGQILTPFE 120
 QY 121 DTEVGGRALHSILNAAIMSVIWMITLLVLYKRCYKVIHAMIISLLLPFFSFI 180
 Db 121 DTEVGGRALHSILNAAIMSVIWMITLLVLYKRCYKVIHAMIISLLLPFFSFI 180
 QY 181 YLGEVFTYVAVDYITVALLINFGVGMISIHMKGRLPLQAYIIMISALMALVFIKY 240
 Db 181 YLGEVFTYVAVDYITVALLINFGVGMISIHMKGRLPLQAYIIMISALMALVFIKY 240
 QY 241 LPEWTAMLIYAVISYVLYAVLCLKGRLMVEYTAQRNTELPALISSTWMLVNMAL 300
 Db 241 LPEWTAMLIYAVISYVLYAVLCLKGRLMVEYTAQRNTELPALISSTWMLVNMAL 300
 QY 301 GDPAPQRVRSKNSKNAESTERESQDTVAENDOGGSEMEARQDSHLGHRSTPSRAA 360
 Db 301 GDPAPQRVRSKNSKNAESTERESQDTVAENDOGGSEMEARQDSHLGHRSTPSRAA 360
 QY 361 VOELSSITLAGEDEEENGVLGLGDFIFYSVLGKASATASGMNTTICFVALILGLCL 420
 Db 361 VOELSSITLAGEDEEENGVLGLGDFIFYSVLGKASATASGMNTTICFVALILGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPMDOIAFRQFYI 467
 Db 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPMDOIAFRQFYI 467

RESULT 5

AAW23964
 ID AAW23964 standard; protein: 467 AA.

XX
 AC AAW23964;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DB Human presentin-1.
 XX
 KW Presentin-1; p51 gene; human; familial Alzheimer's disease; PAD;
 KW cerebral haemorrhage; schizophrenia; depression; epilepsy;
 KW mental retardation; diagnosis; therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 26..29 /note= "residue 26-29 deletion, resulting from
 FT alternative splicing"
 FT Misc-difference 79 /note= "Ala73Xaa mutation site"
 FT Domain 82..100 /label= TM1
 FT /note= "transmembrane domain 1"
 FT Misc-difference 82 /note= "Val82Leu mutation site"
 FT Misc-difference 96

FT Domain /note= "Val196Phe mutation site"
 FT 101..132 /label= TM1-2
 FT /note= "hydrophilic loop"
 FT Misc-difference 115 /note= "Tyr115His mutation site"
 FT 133..154 /label= TM2
 FT /note= "transmembrane domain 2"
 FT Misc-difference 139 /note= "Met139Val mutation site"
 FT 139 /note= "Met139Thr mutation site"
 FT Misc-difference 143 /note= "Met139Thr mutation site"
 FT 143 /note= "Met139Thr mutation site"
 FT Misc-difference 146 /note= "Met146Val mutation site"
 FT 146 /note= "Met146Leu mutation site"
 FT Misc-difference 155..163 /note= "Met146Leu mutation site (Claim 18)"
 FT 155..163 /label= TM2-3
 FT /note= "hydrophilic loop"
 FT Misc-difference 163 /note= "His163Tyr mutation site"
 FT 163 /note= "His163Arg mutation site"
 FT Domain 164..183 /label= TM3
 FT /note= "transmembrane domain 3"
 FT Misc-difference 171 /note= "Leu171Pro mutation site (Claim 18)"
 FT 171 /note= "Phe117Ser mutation site (Claim 1)"
 FT Domain 184..194 /label= TM3-4
 FT /note= "hydrophilic loop"
 FT 195..212 /label= TM4
 FT /note= "transmembrane domain 4"
 FT Misc-difference 209 /note= "Gly209Val mutation site"
 FT 209 /note= "Ile211Thr mutation site"
 FT Domain 213..220 /label= TM4-5
 FT /note= "hydrophilic loop"
 FT 221..238 /label= TM5
 FT /note= "transmembrane domain 5"
 FT Misc-difference 231 /note= "Ala231Thr mutation site"
 FT 231 /note= "Tyr239Ser mutation site"
 FT Domain 239..243 /label= TM5-6
 FT /note= "hydrophilic loop"
 FT 244..262 /label= TM6
 FT /note= "transmembrane domain 6"
 FT Misc-difference 246 /note= "Ala246Glu mutation site"
 FT 246 /note= "Asp257Ala mutation site, associated with residue
 FT 257 /note= "Asp257Ala mutation site, associated with residue
 FT 258-290 deletion (Claim 1)"
 FT Misc-difference 258..290 /note= "residue 258-290 deletion mutant, associated with
 FT Asp257Ala mutation (Claim 1)"
 FT 260 /note= "Ala260Val mutation site (Claim 18)"
 FT 263..407 /label= TM6-7
 FT /note= "hydrophilic loop"
 FT Misc-difference 263 /note= "Cys263Arg mutation site (Claim 18)"
 FT 264

FT	Misc-difference	267	/note= "Pro264Leu mutation site (Claim 18) "
FT	Misc-difference	280	/note= "Pro267Ser mutation site (Claim 18) "
FT	Misc-difference	280	/note= "Glu280Gly mutation site (Claim 18) "
FT	Misc-difference	285	/note= "Glu280Ala mutation site (Claim 18) "
FT	Misc-difference	286	/note= "Ala285Val mutation site (Claim 18) "
FT	Misc-difference	291..319	/note= "Leu286Val mutation site (Claim 18) "
FT	Misc-difference	322	/note= "residue 291-319 deletion site"
FT	Misc-difference	384	/note= "Leu322Val mutation site (Claim 18) "
FT	Misc-difference	392	/note= "Gly384Ala mutation site"
FT	Domain	408..428	/note= "Leu392Val mutation site (Claim 18) "
FT	Domain	408..428	/label= TW8
FT	Misc-difference	410	/note= "transmembrane domain 8"
FT	Misc-difference	439	/note= "Cys410Tyr mutation site (Claim 18) "
FT	Misc-difference	439	/note= "Ile439Val mutation site (Claim 1) "
XX	WO9801549-A2.		
PD	15-JAN-1998.		
XX	04-JUL-1997;	97WO-CA000475.	
XX	05-JUL-1996;	96US-0021673P.	
PR	12-JUL-1996;	96US-0021700P.	
PR	08-NOV-1996;	96US-0029885P.	
PR	02-JAN-1997;	97US-0034550P.	
XX	(TUTOR) UNIV TORONTO GOVERNING COUNCIL.		
PA	(HSCR-) HSC RES & DEV LP.		
XX	St George- Hyslop PH, Fraser PE, Rommens JM;		
XX	WP1: 1998-286355/25.		
DR	N-PSDB; AA004666.		
XX	New isolated mutant presenilin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening.		
XX	Claim 1; Page 180-182; 238pp; English.		
XX	This polypeptide comprises human presenilin-1 (hPS1). Its amino acid sequence was deduced from an isolated cDNA clone (see AA004666). Another hPS1 sequence (see AA023965) results from alternative splicing of the hPS1 mRNA transcript. A murine PS1 homologue (see AA023966) and a human presenilin-2 protein (see AA023967) are also provided. Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as cerebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or derived from the presenilins is made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or modulate the activity of a presenilin protein, and methods for identifying substances that affect the interaction of a presenilin-interacting protein with a presenilin protein are also disclosed		
XX	Sequence 467 AA;		

99.5%; Score 2378; DB 2; Length 467;

[illegible]

XX 14-NOV-2000 (first entry)
 XX Amino acid sequence of human presenilin 1 polypeptide.
 DE Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hNRPAP;
 XX Human; plakophilin related armidillo protein; Alzheimer's disease;
 KM Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke;
 KM multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
 KM motor neuron disease; peripheral neuropathy; neuropathy; diabetes;
 KM spinal cord injury; facial nerve crush.
 XX Homo sapiens.
 OS WO200047615-A2.
 XX 17-AUG-2000.
 PD 11-FEB-2000; 2000WO-CA000126.
 XX PF 12-FEB-1999; 99US-0119835P.
 XX PR (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 PA St George- Hyslop PH, Fraser PE;
 XX WPI; 2000-524531/47.
 XX Stimulation of nerve cell growth using human Neural Plakophilin Related
 PT Armidillo Protein (hNRPAP) polypeptide, useful for the treatment of
 PT diseases such as Alzheimer's, Parkinson's, and stroke.
 XX PS Disclosure: Page 19-20; 33pp; English.
 CC The present sequence represents a human presenilin 1 (PS1) polypeptide.
 CC Human Neural Plakophilin Related Armidillo Protein (hNRPAP) polypeptide
 CC is known to interact with PS1 and PS2. The specification describes a
 CC method for stimulating the growth of nerve cells, comprising contacting
 CC them with hNRPAP. The hNRPAP polypeptide and polynucleotide are useful
 CC for treating nerve damage caused by a variety of diseases or physical
 CC traumas, including Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated
 CC with stroke, neural paropathy, motor neuron diseases, sciatic crush,
 CC peripheral neuropathy, neuropathy associated with diabetes, spinal cord
 CC injuries and facial nerve crush
 CC
 CC Sequence 467 AA;
 SQ
 Query Match 99.5%; Score 2378; DB 3; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSYFONAMQSEDNHLSNTRVSONDRERQEHNDRLSGHPPLSNGRPQGNR 60
 DB 1 MTELPAPLSYFONAMQSEDNHLSNTRVSONDRERQEHNDRLSGHPPLSNGRPQGNR 60
 QY 61 QVDEDEDEDELTKYAKAVIMLFVPVTLQMVVVAATISVSFRRKQGLLYTPTFE 120
 DB 61 QVDEDEDEDELTKYAKAVIMLFVPVTLQMVVVAATISVSFRRKQGLLYTPTFE 120
 QY 121 DTEIVGQALSHLSILAAIMISIVTMTLLVLYKRCYKIHMLTISSLLFFPSFI 180
 DB 121 DTEIVGQALSHLSILAAIMISIVTMTLLVLYKRCYKIHMLTISSLLFFPSFI 180
 QY 121 DTEIVGQALSHLSILAAIMISIVTMTLLVLYKRCYKIHMLTISSLLFFPSFI 180
 DB 121 DTEIVGQALSHLSILAAIMISIVTMTLLVLYKRCYKIHMLTISSLLFFPSFI 180
 QY 181 YLGEVFKTYNVAVDITVALLIMNGVGMISIMKGLRLQOAYLIMISLALVPIKY 240
 DB 181 YLGEVFKTYNVAVDITVALLIMNGVGMISIMKGLRLQOAYLIMISLALVPIKY 240
 QY 241 LPENTAMTILAVISYVDLVAIVLCKGPLRLMVEAQENETLFPALITYSSIMVWLVMAE 300
 DB 241 LPENTAMTILAVISYVDLVAIVLCKGPLRLMVEAQENETLFPALITYSSIMVWLVMAE 300
 QY 301 GDPKQKRVSKSKNAESTERESODTYAENDDGGFSEMEFAQRDSHLGHPRSTPESRAA 360
 DB 301 GDPKQKRVSKSKNAESTERESODTYAENDDGGFSEMEFAQRDSHLGHPRSTPESRAA 360

DB 301 GDPKQKRVSKSKNAESTERESODTYAENDDGGFSEMEFAQRDSHLGHPRSTPESRAA 360
 QY 361 VOELSSSIIAGDEPPEEGVGLGDFIFYSVLVGRXSATASGMWNTTICFVAILIGLCU 420
 DB 361 VOELSSSIIAGDEPPEEGVGLGDFIFYSVLVGRXSATASGMWNTTICFVAILIGLCU 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFFYFATDYLVQPFMDQLAFHQFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFFYFATDYLVQPFMDQLAFHQFYI 467
 RESULT 9
 AAE10798
 ID AAE10798 standard; protein; 467 AA.
 XX AAE10798;
 AC 18-DEC-2001 (first entry)
 DT Human presenilin-1 (PS-1) protein.
 XX Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
 KM neurodegenerative disease; Alzheimer's disease; noctropic; prophylaxis;
 KM neuronal disorder; cognitive disorder.
 XX Homo sapiens.
 OS WO200167097-A2.
 XX 13-SEP-2001.
 PD 09-MAR-2001; 2001WO-GB001059.
 XX 10-MAR-2000; 2000GB-00005895.
 PR (GLAX) GLAXO GROUP LTD.
 PA Hale RS, Rowley A, Blackstock W;
 XX WPI; 2001-589954/66.
 XX N-PSDB; AAD18120.
 DR Identifying presenilin or catenin p120 activity modulator useful for
 PT modulating presenilin-catenin p120 interaction and thus for treating
 PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
 PT cognitive function.
 XX Example 1; Page 41-42; 48pp; English.
 PS The invention relates to a method for identifying modulators of
 CC presenilin and catenin p120. Modulators of catenin p120 and presenilin
 CC are useful for the treatment and prophylaxis of disorders that is
 CC responsive to modulation of presenilin/catenin p120 activity. In
 CC particular, neuronal disorders such as cognitive disorders and
 CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNA
 CC are useful for identifying mutations in catenin p120 genes.
 CC Identification of such mutations assist in the diagnosis of or
 CC susceptibility to Alzheimer's or other conditions associated with
 CC presenilin and in assessing the physiology of such disorders. Catenin
 CC p120 DNA are also used in hybridisation studies to monitor expression of
 CC p120 genes and in particular for up or down regulation of catenin p120
 CC expression. The present sequence is human presenilin-1 (PS-1) protein
 CC
 CC Sequence 467 AA;
 SQ
 Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTELPAPLSYFONAMQSEDNHLSNTRVSONDRERQEHNDRLSGHPPLSNGRPQGNR 60
 DB 1 MTELPAPLSYFONAMQSEDNHLSNTRVSONDRERQEHNDRLSGHPPLSNGRPQGNR 60

CC the treatment or prophylaxis of Alzheimer's disease. The KIAA0253
 CC polynucleotide and KIAA0253 polypeptide are useful in the treatment,
 CC prophylaxis or diagnosis of Alzheimer's disease

XX
 SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSNR 60
 DB 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSNR 60
 QY 61 QVVEDEDEDEBELTLKYGAKVIMLFVPTLCMVVVAATIKSVSYTRKDGQLIYTPFTE 120
 DB 61 QVVEDEDEDEBELTLKYGAKVIMLFVPTLCMVVVAATIKSVSYTRKDGQLIYTPFTE 120
 QY 121 DTEIVGQRALHSINAAIMISIVVMTLLVLYKYRCYKVIHMLIISLLLPFSFT 180
 DB 121 DTEIVGQRALHSINAAIMISIVVMTLLVLYKYRCYKVIHMLIISLLLPFSFT 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIMKGPLRQOAYLIMISALMALVFIFY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIMKGPLRQOAYLIMISALMALVFIFY 240
 QY 241 LPEWTAMILIAVISVYDLVAVLCLKGPLRMLVETAOERNETLPFALIYSSSTMVLYNMAE 300
 DB 241 LPEWTAMILIAVISVYDLVAVLCLKGPLRMLVETAOERNETLPFALIYSSSTMVLYNMAE 300
 QY 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHOFYI 467

RESULT 10
 AAG63936
 ID AAG63936 standard; protein; 467 AA.
 AC AAG63936;
 DT 29-OCT-2001 (first entry)
 DE Amino acid sequence of human presenilin 1.
 KW KIAA0253; presenilin; Alzheimer's disease.
 OS Homo sapiens.
 PN WO200167109-A1.
 PD 13-SEP-2001.
 PF 09-MAR-2001; 2001WO-GB001057.
 PR 10-MAR-2000; 2000GB-00005894.
 PA (GLAXO) GLAXO GROUP LTD.
 RI Hale RS, Rowley A, Blackstock W;
 WP1; 2001-522960/57.
 DR N-PSDB; AAH74993.
 PT Identifying a modulator of presenilin function by determining the ability
 of presenilin to bind to a KIAA0253 polypeptide in the presence and
 absence of a test compound, useful in the treatment or prophylaxis of
 Alzheimer's disease.
 PS Disclosure; Page 40-41; 48pp; English.
 CC The present sequence represents human presenilin 1. KIAA0253 binds to
 CC presenilin. The specification describes a method of identifying a
 CC modulator of presenilin function or KIAA0253 function. The method
 CC comprises determining presenilin activity or KIAA0253 activity in the
 CC presence and absence of a test compound, where presenilin activity is
 CC determined by its ability to bind to KIAA0253. A modulator of presenilin
 CC or KIAA0253 polypeptide is useful in the manufacture of a medicament for

CC the treatment or prophylaxis of Alzheimer's disease. The KIAA0253
 CC polynucleotide and KIAA0253 polypeptide are useful in the treatment,
 CC prophylaxis or diagnosis of Alzheimer's disease

XX
 SQ Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSNR 60
 DB 1 MTELPAPLSTYFQNAQMSDNHLSNTVRQONNREQENDRSLGHPPLSNGRQGSNR 60
 QY 61 QVVEDEDEDEBELTLKYGAKVIMLFVPTLCMVVVAATIKSVSYTRKDGQLIYTPFTE 120
 DB 61 QVVEDEDEDEBELTLKYGAKVIMLFVPTLCMVVVAATIKSVSYTRKDGQLIYTPFTE 120
 QY 121 DTEIVGQRALHSINAAIMISIVVMTLLVLYKYRCYKVIHMLIISLLLPFSFT 180
 DB 121 DTEIVGQRALHSINAAIMISIVVMTLLVLYKYRCYKVIHMLIISLLLPFSFT 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIMKGPLRQOAYLIMISALMALVFIFY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNGVGMISIMKGPLRQOAYLIMISALMALVFIFY 240
 QY 241 LPEWTAMILIAVISVYDLVAVLCLKGPLRMLVETAOERNETLPFALIYSSSTMVLYNMAE 300
 DB 241 LPEWTAMILIAVISVYDLVAVLCLKGPLRMLVETAOERNETLPFALIYSSSTMVLYNMAE 300
 QY 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 DB 301 GDPFAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDSDLGPHRSTPESRAA 360
 QY 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 DB 361 VOELSSSIIAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHOFYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFPATDYLVQPFMDQLAFHOFYI 467

RESULT 11
 AAE05466
 ID AAE05466 standard; protein; 467 AA.
 AC AAE05466;
 DT 24-SEP-2001 (first entry)
 DE Human presenilin (PS1) protein.
 KW Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
 KW NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
 KW peripheral neuropathy; motoneuron disorder; neurodegenerative disorder;
 KW Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
 KW Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
 KW nerve deafness; Alzheimer's disease; epilepsy.
 OS Homo sapiens.
 PN WO200151671-A2.
 PD 19-JUL-2001.
 PF 08-JAN-2001; 2001WO-US000536.
 PR 13-JAN-2000; 2000US-0175200P.
 PR 04-JAN-2001; 2001US-00754949.
 PA (SCIO) SCIOS INC.

PI McCarthy J, Cordell B;
 XX MPI: 2001-451872/48.
 DR N-PSDB; AAE05466.
 XX
 PT Identifying inhibitors of neuronal degeneration useful for treating e.g.
 PT Alzheimer's disease, by determining the ability of a compound to induce
 PT nuclear factor kappa B activation, with the involvement of presentin or
 PT Par-4.
 PS
 PS Claim 4; Page 60-61; 66pp; English.
 XX
 CC The invention relates to human Par-4 protein, presentin protein (PS1 and
 CC PS2) and their corresponding DNA molecules. The invention also relates to
 CC a method for identifying inhibitors of neuronal degeneration, comprising
 CC cotransfecting eukaryotic host cells expressing presentin (PS), with a
 CC Par-4 DNA, and an NF-kappa B dependent reporter construct, exposing the
 CC cotransfected cells to a candidate molecule and monitoring the ability of
 CC the candidate molecule to induce NF-kappa B activation. Presentin
 CC proteins participate in nuclear factor kappa B (NF-kappa B) signalling
 CC and activation. The inhibitors of neuronal degeneration are useful for
 CC treating neurodegenerative disorders such as Alzheimer's disease,
 CC Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea,
 CC Down's syndrome, nerve deafness, Meniere's disease and also for treating
 CC peripheral neuropathies, motor neuron disorders such as amyotrophic
 CC lateral sclerosis (ALS), Bell's palsy and various conditions involving
 CC spinal muscular atrophy and paralysis. The present sequence is human
 CC presentin (PS1) protein
 CC
 CC Sequence 467 AA;
 SQ

Query Match 99.5%; Score 2378; DB 4; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONACMSDNHLSNTVRSQNDREHNDRESLGHPPELSNGRPOGNSR 60
 DB 1 MTELPAPLSYFONACMSDNHLSNTVRSQNDREHNDRESLGHPPELSNGRPOGNSR 60
 QY 61 QVEQDEDEDEDELTLYGAKHYIMLFVPTLCMVVVAVATIKSVSPYTRKQGLIYTPFTE 120
 DB 61 QVEQDEDEDEDELTLYGAKHYIMLFVPTLCMVVVAVATIKSVSPYTRKQGLIYTPFTE 120
 QY 121 DTEYGGORALHSILNAALMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 DB 121 DTEYGGORALHSILNAALMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
 QY 241 LPEWTAAILIIVISYDVAVALCKGPLRMVETAOENETLFPALITYSSMTWLVNMAE 300
 DB 241 LPEWTAAILIIVISYDVAVALCKGPLRMVETAOENETLFPALITYSSMTWLVNMAE 300
 QY 301 GDPENQREVSXKSKNAESTERESQDTVAENDDGFSSEMEARQDSHLGPHRSSTPESRAA 360
 DB 301 GDPENQREVSXKSKNAESTERESQDTVAENDDGFSSEMEARQDSHLGPHRSSTPESRAA 360
 QY 361 VOELSSSILAGDEPBERGVKLGDFIFYSYLVNGKASTAGDMWTITACVALLIGLCL 420
 DB 361 VOELSSSILAGDEPBERGVKLGDFIFYSYLVNGKASTAGDMWTITACVALLIGLCL 420
 QY 421 TLLLAIFKALPALPISITFGLVFFATDVLPQMDLAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGLVFFATDVLPQMDLAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGLVFFATDVLPQMDLAFHQFYI 467
 RESULT 12
 AAEI7051
 ID AAEI7051 standard; protein; 467 AA.
 XX
 AC AAEI7051;

XX 18-Apr-2002 (first entry)
 DT
 XX Human mutant presentin 1 (PS1) wild type protein.
 DE
 XX Human; presentin 1; PS1; amyloid precursor protein; APP; drug screening;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
 KW Huntington's disease; amyotrophic lateral sclerosis; Pick's disease;
 KW head injury disease; frontal lobe dementia; cerebellar degeneration;
 KW ischaemic injury; schizophrenia.
 XX
 XX Homo sapiens.
 OS
 XX WC200202601-A2.
 PN
 XX 10-JUN-2002.
 PD
 XX 29-JUN-2001; 2001MO-US016508.
 PF
 XX 30-JUN-2000; 2000US-0215345P.
 XX
 XX (PhAA) PHARMACIA & UPJOHN CO.
 PA
 XX Carter DE, Tomasselli AG;
 PI
 XX MPI: 2002-140082/18.
 DR
 XX Novel isolated mutant presentin 1 and presentin 2 polypeptides, useful
 PT for screening of drugs for treating pathologies associated with aberrant
 PT amyloid precursor protein processing, such as Alzheimer's disease.
 PT
 XX Disclosure; Fig 1; 80pp; English.
 PS
 XX

The invention relates to mutant presentin 1 (PS1) and presentin 2 (PS2)
 CC polypeptides. Presentin are involved in the processing of amyloid
 CC precursor protein (APP) from which major amyloidogenic peptides are
 CC cleaved. Mutant presentins are useful for identifying agents that
 CC modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
 CC presentin is also useful as a target for screening drugs useful in the
 CC treatment of pathologies associated with aberrant amyloid precursor
 CC protein processing, such as Alzheimer's disease, Parkinson's disease,
 CC multiple sclerosis, Huntington's disease, amyotrophic lateral sclerosis,
 CC head injury disease, Pick's disease, frontal lobe dementia, cerebellar
 CC degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
 CC non-human animal is useful for analysing the interaction between APP and
 CC mutant presentin-processing protease in vivo, and for screening anti-
 CC Alzheimer's disease drugs in vivo. A transgenic non-human animal is
 CC useful for analysing the interaction between APP and mutant presentin-
 CC processing protease in vivo, and for screening anti-Alzheimer's disease
 CC drugs in vivo. The present sequence is human PS1 wild type protein
 CC
 CC Sequence 467 AA;
 SQ

Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFONACMSDNHLSNTVRSQNDREHNDRESLGHPPELSNGRPOGNSR 60
 DB 1 MTELPAPLSYFONACMSDNHLSNTVRSQNDREHNDRESLGHPPELSNGRPOGNSR 60
 QY 61 QVEQDEDEDEDELTLYGAKHYIMLFVPTLCMVVVAVATIKSVSPYTRKQGLIYTPFTE 120
 DB 61 QVEQDEDEDEDELTLYGAKHYIMLFVPTLCMVVVAVATIKSVSPYTRKQGLIYTPFTE 120
 QY 121 DTEYGGORALHSILNAALMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 DB 121 DTEYGGORALHSILNAALMISIVVMTLLVLYKRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNVAVDYITVALLIMNFGVGMISIHMKGPLRLOQAVLIMISALMALVFIKY 240

QY 241 LPEWTAMLLAVISYVDLVAVLCKGRLMVLVETAOERNETLPPALIYSTWVWLVNMAE 300
 Db 241 LPEWTAMLLAVISYVDLVAVLCKGRLMVLVETAOERNETLPPALIYSTWVWLVNMAE 300
 QY 301 GDEPAQRVSKSKKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 Db 301 GDEPAQRVSKSKKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILGICL 420
 Db 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILGICL 420
 QY 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOPEMDQLAFHOXYI 467
 Db 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOPEMDQLAFHOXYI 467

RESULT 13
 AAU79416
 ID AAU79416 standard; protein; 467 AA.
 AC AAU79416;
 XX 02-JUL-2002 (first entry)
 DT
 XX Human presenilin-1, PS-1.
 DE
 XX Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;
 KW gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;
 KM neuroprotective; cytoskeletal; cancer.
 XX
 OS Homo sapiens.
 PN MO20022862-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 12-SEP-2001; 2001WO-GB004094.
 XX
 PR 12-SEP-2000; 2000GB-00022333.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Hiles ID, Ellis C;
 XX
 DR WPI; 2002-351896/38.
 XX
 PT Identifying agent that modulates interaction between integrin-linked
 PT kinase and presenilin-1, useful for treating Alzheimer's disease, and
 PT identifying agent that modulates protein kinase B or gamma secretase
 PT activity.
 XX
 PS Disclosure; Page 43-45; 53pp; English.
 XX
 CC The invention relates to identifying an agent modulating interaction
 CC between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
 CC providing ILK, PSI or their functional variants, as first and second
 CC components respectively, contacting the components in the presence of a
 CC test agent under conditions that in absence of the agent, would permit
 CC of modulating the interaction and determining whether the agent is capable
 CC of modulating the interaction between the components. Also included are
 CC the method above where the components are protein kinase beta (PKB),
 CC gamma secretase or their functional variants, test kits for carrying out
 CC the method and an agent identified by the methods. The methods are used
 CC for identifying an agent that modulates interaction between ILK and PSI.
 CC or PKB or gamma-secretase. The agent has therapeutic applications in
 CC treating humans or animals, for treating a host suffering from a
 CC condition associated with an interaction between ILK and PSI, activity of
 CC PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's
 CC disease. The agent is also useful for manufacturing a medicament for use
 CC in treatment of the above mentioned conditions. The present sequence
 CC represents human presenilin-1, PS-1
 XX

SD Sequence 467 AA;
 Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPISYQNAQMSQEDNLSNTVRSQNDNRROEHNDRSLGHPPLSNRPOQNSR 60
 Db 1 MTELPAPISYQNAQMSQEDNLSNTVRSQNDNRROEHNDRSLGHPPLSNRPOQNSR 60
 QY 61 QVRODEDEDEBELTKGAKAVIMLFVPTLCMVVVAATIKSVSFYTRKQGLITYPTE 120
 Db 61 QVRODEDEDEBELTKGAKAVIMLFVPTLCMVVVAATIKSVSFYTRKQGLITYPTE 120
 QY 121 DTEIVGQRAHSHIINAAIMISIVYMTLLVLVLYKRCYKTIHMLIISLLPPSF 180
 Db 121 DTEIVGQRAHSHIINAAIMISIVYMTLLVLVLYKRCYKTIHMLIISLLPPSF 180
 QY 181 YLGEVFKTYNNAVDYITVALLIMNFGVYGMISIMKGPRLQQAAYLIMISALMLVFITY 240
 Db 181 YLGEVFKTYNNAVDYITVALLIMNFGVYGMISIMKGPRLQQAAYLIMISALMLVFITY 240
 QY 241 LPEWTAMLLAVISYVDLVAVLCKGRLMVLVETAOERNETLPPALIYSTWVWLVNMAE 300
 Db 241 LPEWTAMLLAVISYVDLVAVLCKGRLMVLVETAOERNETLPPALIYSTWVWLVNMAE 300
 QY 301 GDEPAQRVSKSKKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 Db 301 GDEPAQRVSKSKKNAESTERESODTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILGICL 420
 Db 361 VOELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILGICL 420
 QY 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOPEMDQLAFHOXYI 467
 Db 421 TLLILAIFKKALPALPISITFGLVYFATDYLVOPEMDQLAFHOXYI 467

RESULT 14
 AA018049
 ID AA018049 standard; protein; 467 AA.
 AC AA018049;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Presenilin protein.
 XX
 XX Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease;
 KM amyloid precursor protein; APP.
 XX
 OS Unidentified.
 PN
 XX US6376239-B1.
 PN
 XX 23-APR-2002.
 PD
 XX 04-APR-1997; 97US-00832867.
 PF
 XX 04-APR-1997; 97US-00832867.
 PR
 XX 04-APR-1997; 97US-00832867.
 XX
 PA (ELBEG-) ELBEGNE GMBH.
 XX
 PI Baumeister R;
 XX
 DR WPI; 2002-478281/51.
 DR N-PSDB; AAL47323.
 XX
 PT Isolated DNA molecule comprising promoter of the sel-12 gene from
 PT Caenorhabditis elegans operably linked to heterologous gene, directs
 PT expression in neural cells and is useful to develop drugs to treat
 PT neuronal disorders.
 PT

XX Claim 2; Fig 4; 78pp; English.
 CC The present invention relates to DNA molecules comprising the promoter of
 CC the sel-12 gene from *Caenorhabditis elegans* operably linked to a
 CC heterologous DNA sequence encoding a protein of interest. The sequence
 CC can be used to develop drugs for the treatment, prevention or delay of a
 CC neuronal disorder. In particular, the neuronal disorder may be familial
 CC Alzheimer's disease. The present sequence is a presentin-1 protein
 CC described in the exemplification of the invention

XX Sequence 467 AA;

Query Match 99.5%; Score 2378; DB 5; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1.4e-233;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQENHDSRLGHPPLNSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQENHDSRLGHPPLNSGRPGNSR 60
 QY 61 QVVEODEEBDEBLTLKYGAKHYIMLFVPTLCMVVVVATIKSVSPYTRDQGLITPPT 120
 DB 61 QVVEODEEBDEBLTLKYGAKHYIMLFVPTLCMVVVVATIKSVSPYTRDQGLITPPT 120
 QY 121 DNETVGORALHSILNAAIMISIVMTLLVLYKRCYKIHAWLIISLLFFFSFI 180
 DB 121 DNETVGORALHSILNAAIMISIVMTLLVLYKRCYKIHAWLIISLLFFFSFI 180
 QY 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMLVFIKY 240
 DB 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMLVFIKY 240
 QY 241 LPEMTAMLIAYISYVDLVAVLCCKPPLMLVETAOERNETLFPALITYSTWMLVNMAB 300
 DB 241 LPEMTAMLIAYISYVDLVAVLCCKPPLMLVETAOERNETLFPALITYSTWMLVNMAB 300
 QY 301 GDEPAQRVRSKNSKNAESTERESODTVAENDDGFSEMEAROSHLPHRSTPESRAA 360
 DB 301 GDEPAQRVRSKNSKNAESTERESODTVAENDDGFSEMEAROSHLPHRSTPESRAA 360
 QY 361 VOELSSSIIAGDEPBERGVKLGDFITFYSVYVKGASATASGDWNTTIACFAVILIGLCL 420
 DB 361 VOELSSSIIAGDEPBERGVKLGDFITFYSVYVKGASATASGDWNTTIACFAVILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOPIYI 467
 DB 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOPIYI 467

RESULT 15

AA05737
 ID AAM05737 standard; protein; 467 AA.

AC AAM05737;

XX 25-MAR-2003 (revised)
 DT 23-JUL-1997 (first entry)
 XX

DE Presentin-1-1 V82L mutation.

XX Presentin-1; human; hpsl-1; hpsl-2; PS-2; integral membrane protein; AD;
 KW familial Alzheimer's disease; cerebral haemorrhage; schizophrania;
 KW depression; antibody; gene expression modulator; therapy; mutuin.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 82
 FT /label= V82L

XX WO9634099-A2.

PD 31-OCT-1996.
 XX
 XX 29-APR-1996; 96MO-CA000263.
 XX
 PR 28-APR-1995; 95US-00431048.
 PR 28-JUN-1995; 95US-00496841.
 PR 31-JUL-1995; 95US-00509359.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
 XX
 PI St George's Hosp PH, Fraser PE, Rommens JM;
 DR WPI; 1996-497631/49.
 XX
 PT New presentin genes - useful for diagnosis, therapy and drug screening
 PT of familial Alzheimer's disease, cerebral disorders, etc.
 PS
 PS Claim 3; Page; 178pp; English.

CC AAM05736-W05760 represent mutated versions of the human presentin-1-1
 CC protein (see AAM05733 for wild type sequence). AAM05734 represents a
 CC different wild type form of presentin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presentins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrania, depression etc., so detection of mutations in the DNA
 CC encoding the wild type sequences can be used for diagnosis of these
 CC diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are useful
 CC as models for drug screening. The antibodies can also be used e.g. for
 CC affinity purification and in immunoassays. (updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX

SQ Sequence 467 AA;

Query Match 99.3%; Score 2375; DB 2; Length 467;
 Best Local Similarity 99.4%; Pred. No. 2.8e-233;
 Matches 464; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQENHDSRLGHPPLNSGRPGNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQENHDSRLGHPPLNSGRPGNSR 60
 QY 61 QVVEODEEBDEBLTLKYGAKHYIMLFVPTLCMVVVVATIKSVSPYTRDQGLITPPT 120
 DB 61 QVVEODEEBDEBLTLKYGAKHYIMLFVPTLCMVVVVATIKSVSPYTRDQGLITPPT 120
 QY 121 DNETVGORALHSILNAAIMISIVMTLLVLYKRCYKIHAWLIISLLFFFSFI 180
 DB 121 DNETVGORALHSILNAAIMISIVMTLLVLYKRCYKIHAWLIISLLFFFSFI 180
 QY 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMLVFIKY 240
 DB 181 YLGEVFKTYNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMLVFIKY 240
 QY 241 LPEMTAMLIAYISYVDLVAVLCCKPPLMLVETAOERNETLFPALITYSTWMLVNMAB 300
 DB 241 LPEMTAMLIAYISYVDLVAVLCCKPPLMLVETAOERNETLFPALITYSTWMLVNMAB 300
 QY 301 GDEPAQRVRSKNSKNAESTERESODTVAENDDGFSEMEAROSHLPHRSTPESRAA 360
 DB 301 GDEPAQRVRSKNSKNAESTERESODTVAENDDGFSEMEAROSHLPHRSTPESRAA 360
 QY 361 VOELSSSIIAGDEPBERGVKLGDFITFYSVYVKGASATASGDWNTTIACFAVILIGLCL 420
 DB 361 VOELSSSIIAGDEPBERGVKLGDFITFYSVYVKGASATASGDWNTTIACFAVILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHOPIYI 467

Fri Apr 9 06:19:30 2004

us-09-785-474a-30.rag

Page 12

Db 421 TTTTTTIFKKALPALPISITFGLVFFATDYLWQPMQLAFFHQFYI 467

Search completed: April 8, 2004, 16:56:31
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 16:58:26 ; Search time 47 Seconds

(without alignments)
2612.596 Million cell updates/sec

Title: US-09-785-474A-30

Perfect score: 2391
Sequence: 1 MTEBPAPUSYFONQMSDN.....ATDVLVQPFMDLAFHQFYI 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2384	99.7	467	9	US-09-785-474-2
3	2379	99.5	467	9	US-09-785-474-32
4	2378	99.5	467	9	US-09-754-949-4
5	2378	99.5	467	9	US-09-878-454A-3
6	2378	99.5	467	9	US-09-895-035-14
7	2378	99.5	467	13	US-10-071-900-1
8	2378	99.5	467	14	US-10-221-254-4
9	2378	99.5	467	15	US-10-180-781-3
10	2378	99.5	467	15	US-10-417-422-4
11	2374	99.3	467	9	US-09-785-474-4
12	2372	98.2	463	9	US-09-895-035-12
13	2348	98.2	463	9	US-09-895-035-12
14	2266	94.8	467	14	US-10-293-000-5
15	1452	60.7	448	9	US-09-878-454A-1

16	1452	60.7	448	13	US-10-071-900-2	Sequence 2, Appli
17	1452	60.7	448	14	US-10-293-000-6	Sequence 6, Appli
18	1452	60.7	448	14	US-10-180-781-2	Sequence 2, Appli
19	1444	60.4	448	9	US-09-754-949-6	Sequence 6, Appli
20	1444	60.4	448	14	US-10-221-254-6	Sequence 6, Appli
21	1444	60.4	448	15	US-10-417-422-6	Sequence 1, Appli
22	798.5	33.4	180	9	US-09-895-035-1	Sequence 8, Appli
23	653	27.3	354	9	US-09-823-153-8	Sequence 6, Appli
24	552.5	23.1	478	12	US-10-425-11-60796	Sequence 47501, A
25	552.5	23.1	481	12	US-10-425-11-47501	Sequence 30637, A
26	377	15.8	80	14	US-10-029-386-30637	Sequence 1227, Ap
27	365	15.3	101	9	US-09-925-299-1227	Sequence 1227, Ap
28	365	15.3	101	10	US-10-051-767-11	Sequence 11, Appl
29	362.5	15.2	129	14	US-10-051-767-10	Sequence 12, Appl
30	361.5	15.1	111	14	US-10-051-767-10	Sequence 12, Appl
31	335	14.0	210	12	US-10-051-767-12	Sequence 196951, A
32	328.5	13.7	233	12	US-10-424-599-196951	Sequence 7, Appl
33	299	12.5	166	14	US-10-051-767-7	Sequence 13, Appl
34	299	12.5	166	14	US-10-051-767-13	Sequence 196783, A
35	278.5	11.6	177	12	US-10-424-599-196783	Sequence 9, Appli
36	246	10.3	74	14	US-10-051-767-9	Sequence 15, Appl
37	246	10.3	74	14	US-10-051-767-15	Sequence 38056, A
38	243.5	10.2	65	9	US-09-864-761-38056	Sequence 6, Appli
39	235.5	9.8	124	15	US-10-411-207-6	Sequence 209024, A
40	231.5	9.7	98	12	US-10-424-599-209024	Sequence 203174, A
41	221	9.2	60	12	US-10-424-599-203174	Sequence 28604, A
42	198	8.3	42	14	US-10-029-386-28604	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
US-09-785-474-30
Sequence 30, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
MASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609,4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-785-474-30

Query Match

Best Similarity 100.0%; Score 2391; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.5e-206; Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPPLSGRPOGNSR 60
 DB 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPPLSGRPOGNSR 60
 QY 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
 DB 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
 QY 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 DB 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 QY 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 241 LPBWTAMLLAVISYVDLVAVLCCKGPLRLMVELTQERNETLFPALISSITVWLVNMAE 300
 DB 241 LPBWTAMLLAVISYVDLVAVLCCKGPLRLMVELTQERNETLFPALISSITVWLVNMAE 300
 QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 DB 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 QY 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 DB 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 QY 421 TLULLAIFKKALPALPISITFGLVFPAFDYLVQPFMDQLAHQFYI 467
 DB 421 TLULLAIFKKALPALPISITFGLVFPAFDYLVQPFMDQLAHQFYI 467

RESULT 2

US-09-785-474-2
 Sequence 2, Application US/09785474
 Patent No. US20010012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/785,474

FILING DATE: 20-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344

FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0609,4180002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-785-474-2

Query Match

Best Similarity 99.7%; Score 2384; DB 9; Length 467;
Best Local Similarity 99.8%; Pred. No. 6.2e-206; Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPPLSGRPOGNSR 60
 DB 1 MTELPAPLSTYFQNAQMSSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPPLSGRPOGNSR 60
 QY 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
 DB 61 QVEODEEEDDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
 QY 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 DB 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 QY 121 DTEYQGRALHSILNAALIMISIVVMTLLVLYKRCYKVIHAWLLISLLFFFSFI 180
 DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 241 LPBWTAMLLAVISYVDLVAVLCCKGPLRLMVELTQERNETLFPALISSITVWLVNMAE 300
 DB 241 LPBWTAMLLAVISYVDLVAVLCCKGPLRLMVELTQERNETLFPALISSITVWLVNMAE 300
 QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 QY 301 GDPEAQRVSKSKNAESTERESQDTVAENDDGFSEMEWQRSDHSGPHRSTPESRAA 360
 DB 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 QY 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 DB 361 VOELSSSIILAGDPEERGVKLGDFIFYSVLVGRASATASGDWNTTIACFVALIIGLCL 420
 QY 421 TLULLAIFKKALPALPISITFGLVFPAFDYLVQPFMDQLAHQFYI 467
 DB 421 TLULLAIFKKALPALPISITFGLVFPAFDYLVQPFMDQLAHQFYI 467

RESULT 3

US-09-785-474-32
 Sequence 32, Application US/09785474
 Patent No. US20010012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH

MASCO, WILMA

TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/785,474
 FILING DATE: 20-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/706,344
 FILING DATE: 30-AUG-1996
 APPLICATION NUMBER: 60/003,054
 FILING DATE: 31-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: KIM, JUDITH U.
 REGISTRATION NUMBER: 40,679
 REFERENCE/DOCKET NUMBER: 0609,4180002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-09-785-474-32

Query Match 99.5%; Score 2379; DB 9; Length 467;
 Best Local Similarity 99.6%; Pred. No. 1,7e-205;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
 QY 61 QVVEODEEDELTLKYGAKHYIMLFVPTLCMVVVVAITIKSVSFYTRKDGOLITPTE 120
 DB 61 QVVEODEEDELTLKYGAKHYIMLFVPTLCMVVVVAITIKSVSFYTRKDGOLITPTE 120
 QY 121 DTEVGOALHSILNAAIMISVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGOALHSILNAAIMISVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 DB 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 QY 241 LPEWTAMLLAVISYDVAVALCKGPLRMLVETAQERNETLFPALIVSSTWMLVNMAL 300
 DB 241 LPEWTAMLLAVISYDVAVALCKGPLRMLVETAQERNETLFPALIVSSTWMLVNMAL 300
 QY 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
 DB 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTACFAVAILIGLCL 420
 QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOFPMDQLAFHOFYI 467
 DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOFPMDQLAFHOFYI 467

RESULT 4
 US-09-754-949-4
 Sequence 4, Application US/09754949
 Patent No. US20020015939A1
 GENERAL INFORMATION:

APPLICANT: MCCARTHY, JUSTIN
 APPLICANT: CORDELL, BARBARA
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
 TITLE OF INVENTION: NEURONAL DEGENERATION
 FILE REFERENCE: SCIOS.012A
 CURRENT APPLICATION NUMBER: US/09/754,949
 CURRENT FILING DATE: 2001-01-04
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-754-949-4

Query Match 99.5%; Score 2378; DB 9; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2,2e-205;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
 DB 1 MTELPAPLSYFQNAQWSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNGRPOGNSR 60
 QY 61 QVVEODEEDELTLKYGAKHYIMLFVPTLCMVVVVAITIKSVSFYTRKDGOLITPTE 120
 DB 61 QVVEODEEDELTLKYGAKHYIMLFVPTLCMVVVVAITIKSVSFYTRKDGOLITPTE 120
 QY 121 DTEVGOALHSILNAAIMISVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 DB 121 DTEVGOALHSILNAAIMISVIYVMTLLVLYKRCYKVIHAWLIISLLFFPSFI 180
 QY 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 DB 181 YLGEVFTYNAVDYITVALLIMNFGVGMISIMKGPLRLQOAYLIMISALMAVFIKY 240
 QY 241 LPEWTAMLLAVISYDVAVALCKGPLRMLVETAQERNETLFPALIVSSTWMLVNMAL 300
 DB 241 LPEWTAMLLAVISYDVAVALCKGPLRMLVETAQERNETLFPALIVSSTWMLVNMAL 300
 QY 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
 DB 301 GDPAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRSHLGPHERSTPESRAA 360
 QY 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTACFAVAILIGLCL 420
 DB 361 VOELSSSILAGEDEPERGVKLGDFIFYSYLVGKASATASGDMNTTACFAVAILIGLCL 420
 QY 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOFPMDQLAFHOFYI 467
 DB 421 TLLLAIFKKALPALPISITFGLVFPATDYLVOFPMDQLAFHOFYI 467

RESULT 5
 US-09-878-454A-3
 Sequence 3, Application US/09878454A
 Patent No. US20020064828A1
 GENERAL INFORMATION:
 APPLICANT: Monteiro, et al.
 TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentlin
 FILE REFERENCE: 4115-161
 CURRENT APPLICATION NUMBER: US/09/878,454A
 CURRENT FILING DATE: 2001-06-11
 PRIOR FILING DATE: 2000-06-11
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 3
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-878-454A-3

Query Match 99.5%; Score 2378; DB 9; Length 467;

Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120
QY 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
QY 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
QY 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360
Db 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360
QY 361 VOELSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
Db 361 VOELSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLULLAIFKKALPALPISITFGVLFYFATDYLQPFMDQLAFHQFYI 467
Db 421 TLULLAIFKKALPALPISITFGVLFYFATDYLQPFMDQLAFHQFYI 467

RESULT 6
US-09-895-035-14
Sequence 14, Application US/09895035
Patent No. US2002008211A1
GENERAL INFORMATION:
APPLICANT: Patterson, Chandra
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN PRESENTILIN VARIANT
FILE REFERENCE: PC-0047 CIP
CURRENT APPLICATION NUMBER: US/09/895, 035
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/116, 640
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2002008211A1 g1709856
US-09-895-035-14

Query Match 99.5%; Score 2378; DB 9; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120

QY 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
QY 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
QY 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360
Db 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360
QY 361 VOELSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
Db 361 VOELSSILAGEPBERGVKLGDFIFYSVLVGKASATASGDMNTTACFAVAILIGLCL 420
QY 421 TLULLAIFKKALPALPISITFGVLFYFATDYLQPFMDQLAFHQFYI 467
Db 421 TLULLAIFKKALPALPISITFGVLFYFATDYLQPFMDQLAFHQFYI 467

RESULT 7
US-10-071-900-1
Sequence 1, Application US/10071900
Publication No. US20020127541A1
GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter H.
APPLICANT: Rommens, Johanna
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
FILE REFERENCE: 1034/1F810-US1
CURRENT APPLICATION NUMBER: US/10/071, 900
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/227, 725
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 467
TYPE: PRT
ORGANISM: Homo Sapien
US-10-071-900-1

Query Match 99.5%; Score 2378; DB 13; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
Db 1 MTELPALSYFQNAQSEDNHLSNTVRSQNDNRERQEHNDRLSGHPEPLSNRPGQNSR 60
QY 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120
Db 61 QVVEQDEEEDBELTLKYGAGVIMLFVPTLQVWVVAATIKSYFYTRKDGQLIYPTPE 120
QY 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
Db 121 DTEVQORALHSLINAAIMISVIVMTILLVLYKRCYKVIHAWLIISLLFFPSFI 180
QY 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
Db 181 YLGEVFKTYNVAVDYITVALLINFGVGMISIMHGKPLRLQQAYLIMISALMAVFIKY 240
QY 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
Db 241 LPEWTAMLIAVISVDLVAVLCLKGFLRMVETAGERNETLFPALISSTWMLVNMAB 300
QY 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360
Db 301 GDPBQRRVSKNSKNAESTERESQDTVAENDGCFSEWEAQRDShLGPBRSTPESRAA 360


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Db      301 GDBEQRVRVSKNSKYNASTERSQDTVAENDDGGSEEMEQORSHLQPHRSIPESRAA 360
Qy      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420
Db      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420
Qy      421 TLLLLAIFKKALPALPISTTFGLVFFAFDYLVOPEMDQLAFHOFYI 467
Db      421 TLLLLAIFKKALPALPISTTFGLVFFAFDYLVOPEMDQLAFHOFYI 467

RESULT 8
US-10-221-254-4
; Sequence 4, Application US/10221254
; Publication No. US20030113811A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: PG3950USW
; CURRENT APPLICATION NUMBER: US/10/221,254
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0005894.1
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 467
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-221-254-4

Query Match          99.5%; Score 2378; DB 14; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MTELPAPLSYFONQMSQEDNHLSTNTRSQNDNREROEHNDRSLGHPEPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFONQMSQEDNHLSTNTRSQNDNREROEHNDRSLGHPEPLSNGRPOGNSR 60
Qy      61 QVVEODEEBEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKXGOLITPTE 120
Db      61 QVVEODEEBEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKXGOLITPTE 120
Qy      121 DTEVGOALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Db      121 DTEVGOALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Qy      181 YLGEVFKTVNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
Db      181 YLGEVFKTVNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
Qy      241 LPBWTAMLILAVISYVDLVAVLCCKGPLRMLVETAOERNETLFPALIVYSTWVLVYMAE 300
Db      241 LPBWTAMLILAVISYVDLVAVLCCKGPLRMLVETAOERNETLFPALIVYSTWVLVYMAE 300
Qy      301 GDBEQRVRVSKNSKYNASTERSQDTVAENDDGGSEEMEQORSHLQPHRSIPESRAA 360
Db      301 GDBEQRVRVSKNSKYNASTERSQDTVAENDDGGSEEMEQORSHLQPHRSIPESRAA 360
Qy      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420
Db      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420
Qy      421 TLLLLAIFKKALPALPISTTFGLVFFAFDYLVOPEMDQLAFHOFYI 467
Db      421 TLLLLAIFKKALPALPISTTFGLVFFAFDYLVOPEMDQLAFHOFYI 467

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GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
Schellenberg, Gerard D.
Wasco, Wilma
Levy-Lahad, Ephrat
Bird, Thomas D.
Galas, David J.
TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Ave, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/180,781
FILING DATE: 24-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 920010.571C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-180-781-3

Query Match          99.5%; Score 2378; DB 14; Length 467;
Best Local Similarity 99.6%; Pred. No. 2.2e-205;
Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MTELPAPLSYFONQMSQEDNHLSTNTRSQNDNREROEHNDRSLGHPEPLSNGRPOGNSR 60
Db      1 MTELPAPLSYFONQMSQEDNHLSTNTRSQNDNREROEHNDRSLGHPEPLSNGRPOGNSR 60
Qy      61 QVVEODEEBEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKXGOLITPTE 120
Db      61 QVVEODEEBEDELTKYGAHVIMLFVPTLCMVVVVATIKSVFYTRKXGOLITPTE 120
Qy      121 DTEVGOALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Db      121 DTEVGOALHSILNAAIMISVIVMTLLVLYKRCYKVIHAWLIISLLFFFSFI 180
Qy      181 YLGEVFKTVNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
Db      181 YLGEVFKTVNAVADYITVALLINFGVGMISIHMKGPLRLOQAYLIMISALMALVFIKY 240
Qy      241 LPBWTAMLILAVISYVDLVAVLCCKGPLRMLVETAOERNETLFPALIVYSTWVLVYMAE 300
Db      241 LPBWTAMLILAVISYVDLVAVLCCKGPLRMLVETAOERNETLFPALIVYSTWVLVYMAE 300
Qy      301 GDBEQRVRVSKNSKYNASTERSQDTVAENDDGGSEEMEQORSHLQPHRSIPESRAA 360
Db      301 GDBEQRVRVSKNSKYNASTERSQDTVAENDDGGSEEMEQORSHLQPHRSIPESRAA 360
Qy      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420
Db      361 VOELSSSIILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDMNTTIACFVAIIIGLCL 420

```

QY 421 TLLLLAIFKKALPALPISITFGVFPATDVLVQPFMDQLAFHQFYI 467
 Db 421 TLLLLAIFKKALPALPISITFGVFPATDVLVQPFMDQLAFHQFYI 467

RESULT 10

US-10-417-422-4
 ; Sequence 4, Application US/10417422
 ; Publication No. US20030219720A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCARTHY, JUSTIN
 ; APPLICANT: CORDELL, BARBARA
 ; APPLICANT: SCIOS, INC.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
 ; TITLE OF INVENTION: NEURONAL DEGENERATION
 ; FILE REFERENCE: SCIOS.012C1
 ; CURRENT APPLICATION NUMBER: US/10/417.422
 ; CURRENT FILING DATE: 2003-04-14
 ; PRIOR APPLICATION NUMBER: 09/754949
 ; PRIOR FILING DATE: 2001-02-04
 ; PRIOR APPLICATION NUMBER: 60/175200
 ; PRIOR FILING DATE: 2000-01-10
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIEN
 US-10-417-422-4

Query Match 99.5%; Score 2378; DB 15; Length 467;
 Best Local Similarity 99.6%; Pred. No. 2.2e-205;
 Matches 465; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRREOEHNDRSLGHPPLSNRPOGNSR 60
 Db 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRREOEHNDRSLGHPPLSNRPOGNSR 60
 QY 61 QVQDEDEDEDELTKYGAQKIVMLFVPVTLQWVVVAATIKSVSFYTRKDGQLIYPTPE 120
 Db 61 QVQDEDEDEDELTKYGAQKIVMLFVPVTLQWVVVAATIKSVSFYTRKDGQLIYPTPE 120
 QY 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 QY 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 QY 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 QY 361 VQELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 Db 361 VQELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 QY 421 TLLLLAIFKKALPALPISITFGVFPATDVLVQPFMDQLAFHQFYI 467
 Db 421 TLLLLAIFKKALPALPISITFGVFPATDVLVQPFMDQLAFHQFYI 467

RESULT 11
 US-09-785-474-4
 ; Sequence 4, Application US/09785474
 ; Patent No. US20010012626A1
 ; GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH
 ;
 ; TITLE OF INVENTION: Genetic Alterations Related To Familial
 ; Alzheimer's Disease
 ;
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/785.474
 ; FILING DATE: 20-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/706,344
 ; FILING DATE: 30-AUG-1996
 ; APPLICATION NUMBER: 60/003,054
 ; FILING DATE: 31-AUG-1995
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KIM, JUDITH U.
 ; REGISTRATION NUMBER: 40,679
 ; REFERENCE/DOCKET NUMBER: 0609.4180002
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ;
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 ;
 ; US-09-785-474-4
 ;
 ; Query Match 99.3%; Score 2374; DB 9; Length 467;
 ; Best Local Similarity 99.6%; Pred. No. 4.9e-205;
 ; Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRREOEHNDRSLGHPPLSNRPOGNSR 60
 Db 1 MTELPAPLSYFQNAQMSQEDNHLSTVRSQNDNRREOEHNDRSLGHPPLSNRPOGNSR 60
 QY 61 QVQDEDEDEDELTKYGAQKIVMLFVPVTLQWVVVAATIKSVSFYTRKDGQLIYPTPE 120
 Db 61 QVQDEDEDEDELTKYGAQKIVMLFVPVTLQWVVVAATIKSVSFYTRKDGQLIYPTPE 120
 QY 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 QY 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 Db 121 DTEIVGQRAHSIINAAMISIVVMTLLVLYKYRCYKVIHAWLLISSLLLPFSFI 180
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 Db 181 YLGEVFKTYNVAVDYITVALLINMGVGMISIMHKGPLRLOQAVLIMISALMALVFIKY 240
 QY 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 QY 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 Db 241 LPEWTAMILLAVISYVDLVAVLCKGPLRLMLETQOERNETLPPALYSSSTMWLVNMAE 300
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 QY 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 Db 301 GDPBAQRVSKSKNAESTERESQDTVAENDDGFSEWEAQRDLSHGPRSTPESRAA 360
 QY 361 VQELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420
 Db 361 VQELSSSILAGEDEPERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVAIILIGLCL 420

QY 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQAFHQFYI 467

RESULT 12

US-09-785-474-28
 Sequence 28, Application US/09785474
 Patent No. US20010012626A1

GENERAL INFORMATION:

APPLICANT: TANZI, RUDOLPH
 MASCO, WILLIAM
 TITLE OF INVENTION: Genetic Alterations Related To Familial
 Alzheimer's Disease
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/785,474
 FILING DATE: 20-Feb-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/706,344
 FILING DATE: 30-AUG-1996
 APPLICATION NUMBER: 60/003,054
 FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.
 REGISTRATION NUMBER: 40,679
 REFERENCE/DOCKET NUMBER: 0609.4180002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-09-785-474-28

Query Match 99.2%; Score 2372; DB 9; Length 467;

Best Local Similarity 99.6%; Pred. No. 7.5e-205;
 Matches 465; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 QY 61 QVEODEEEDBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFYTRDGQLIYTPFTE 120
 DB 61 QVEODEEEDBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFYTRDGQLIYTPFTE 120
 QY 121 DTEYVQGRALSHILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 DB 121 DTEYVQGRALSHILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240

QY 241 LPEWTAMLLIAVISYVDLVAVLCLKGPLRLVETARQERNETLFPALITYSTMTWLVNMAE 300
 DB 241 LPEWTAMLLIAVISYVDLVAVLCLKGPLRLVETARQERNETLFPALITYSTMTWLVNMAE 300
 QY 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 QY 361 VOELSSSIIILAGEDEEERGVKLGDFIFYSVLVGRKASATASGDMNTTIAQFVALILGLCL 420
 DB 361 VOELSSSIIILAGEDEEERGVKLGDFIFYSVLVGRKASATASGDMNTTIAQFVALILGLCL 420
 QY 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQAFHQFYI 467
 DB 421 TLLLAIFKALPALPISITFGVFPATDYLQPFMDQAFHQFYI 467

RESULT 13

US-09-895-035-12
 Sequence 12, Application US/09895035
 Patent No. US20020082211A1

GENERAL INFORMATION:

APPLICANT: Patterson, Chandra
 Murtty, Lynn B.
 TITLE OF INVENTION: HUMAN PRESENTILIN VARIANT
 FILE REFERENCE: PC-0047 CIP
 CURRENT APPLICATION NUMBER: US/09/895,035
 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: 09/116,640
 PRIOR FILING DATE: 1998-07-16
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PERL Program

SEQ ID NO 12

LENGTH: 463
 TYPE: PRT
 ORGANISM: Homo sapiens
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244638
 US-09-895-035-12

Query Match 98.2%; Score 2348; DB 9; Length 463;
 Best Local Similarity 98.7%; Pred. No. 1.1e-202;
 Matches 461; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 60
 DB 1 MTELPAPLSYFQNAQMSDNHLSNTVRSONDRERQENHNDRLSGHPEPLSNRPGQNSR 56
 QY 61 QVEODEEEDBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFYTRDGQLIYTPFTE 120
 DB 57 QVEODEEEDBELTLKYGAKHYIMLFVPTLCMVVVAATIKSVSFYTRDGQLIYTPFTE 116
 QY 121 DTEYVQGRALSHILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 180
 DB 117 DTEYVQGRALSHILNAAMISIVVMTLLVLYKRCYKVIHAWLIISLLLPFSFI 176
 QY 181 YLGEVFKTYNAVDYITVALLIMNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 177 YLGEVFKTYNAVDYITVALLIMNFGVGMISIHMKGPLRLQOAYLIMISALMALVFIKY 236
 QY 241 LPEWTAMLLIAVISYVDLVAVLCLKGPLRLVETARQERNETLFPALITYSTMTWLVNMAE 300
 DB 237 LPEWTAMLLIAVISYVDLVAVLCLKGPLRLVETARQERNETLFPALITYSTMTWLVNMAE 296
 QY 301 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 360
 DB 297 GDPEAQRVSKNSKNAESTERESQDTVAENDDGFSEWEAQRDHLGPHRSTPESRAA 356
 QY 361 VOELSSSIIILAGEDEEERGVKLGDFIFYSVLVGRKASATASGDMNTTIAQFVALILGLCL 420
 DB 357 VOELSSSIIILAGEDEEERGVKLGDFIFYSVLVGRKASATASGDMNTTIAQFVALILGLCL 416

QY 421 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 467
 DB 417 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 463

RESULT 14

US-10-293-000-5
 ; Sequence 5, Application US/10293000
 ; Publication No. US20030175278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monteiro, Mervyn J.
 ; APPLICANT: Mah, Alex L.
 ; APPLICANT: Perry, George
 ; TITLE OF INVENTION: UBIQUILIN, A PRESENTILIN INTERACTOR AND METHODS OF USING SAME
 ; FILE REFERENCE: 4115-175
 ; CURRENT APPLICATION NUMBER: US/10/293,000
 ; CURRENT FILING DATE: 2003-04-01
 ; PRIOR APPLICATION NUMBER: US 60/338,549
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-000-5

Query Match 94.8%; Score 2266; DB 14; Length 467;
 Best Local Similarity 94.6%; Pred. No. 2,66-195;
 Matches 442; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTELPAPISYFQNAQMSDNHLSNTVRSQNDNREROEHDRSLGHEPEPLNSGRPOGNSR 60
 DB 1 MTELPAPISYFQNAQMSDNHLSNTVRSQNDNREROEHDRSLGHEPEPLNSGRPOGNSG 60
 QY 61 QVDEDEDEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKQGLIYPTFE 120
 DB 61 PVERDEDEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKQGLIYPTFE 120
 QY 121 DTEVGRALHSILNAAIMISIVVMTLLVLYKYRCYKVIHAMLIISSLLFFPSFI 180
 DB 121 DTEVGRALHSILNAAIMISIVVMTLLVLYKYRCYKVIHAMLIISSLLFFPSFI 180
 QY 181 YLGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 DB 181 YLGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 240
 QY 241 LPWTAMLILAVISYDVAVLCCKGPLRMLVETAOERNETLFPALIISSSTMVLVMAE 300
 DB 241 LPWTAMLILAVISYDVAVLCCKGPLRMLVETAOERNETLFPALIISSSTMVLVMAE 300
 QY 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFSSEWMAQRDLSHGHRSTPESRAA 360
 DB 301 GDPFAQRVSKSKNAESTERESQDTVAENDDGFSSEWMAQRDLSHGHRSTPESRAA 360
 QY 361 VQESSSTIAGDEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
 DB 361 VQESSSTIAGDEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 420
 QY 421 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 467
 DB 421 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 467

RESULT 15

US-09-878-454A-1
 ; Sequence 1, Application US/09878454A
 ; Patent No. US20020064828A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monteiro, et al.
 ; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentilin

FILE REFERENCE: 4115-161
 ; CURRENT APPLICATION NUMBER: US/09/878,454A
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: 60/210,939
 ; PRIOR FILING DATE: 2000-06-11
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-878-454A-1

Query Match 60.7%; Score 1452; DB 9; Length 448;
 Best Local Similarity 65.2%; Pred. No. 5e-122;
 Matches 304; Conservative 40; Mismatches 80; Indels 42; Gaps 8;

QY 3 ELPLPAPISYFQNAQMSDNHLSNTVRSQNDNREROEHDRSLGHEPEPLNSGRPOGNSRQ 61
 DB 24 ESPTRSCOEGRQDEGENTQOMRSOENDEGEDPDRYCSGVF-----GRPG----- 74
 QY 62 VDEDEDEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKQGLIYPTFE 121
 DB 75 -----LEDELTLKYGAKHVMLEFVPTLCMVVVVATIKSVSFYTRKQGLIYPTFE 127
 QY 122 TETVGRALHSILNAAIMISIVVMTLLVLYKYRCYKVIHAMLIISSLLFFPSFI 181
 DB 128 TETVGRALHSILNAAIMISIVVMTLLVLYKYRCYKVIHAMLIISSLLFFPSFI 187
 QY 182 LGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 241
 DB 188 LGEVFKYVNAVYITVALLINMGVGMISIMKGPLRLQOAYLIMISALMALVFIKY 247
 QY 242 LPWTAMLILAVISYDVAVLCCKGPLRMLVETAOERNETLFPALIISSSTMVLVMAE 301
 DB 248 PMSAMVILGASVYDVAVLCCKGPLRMLVETAOERNETLFPALIISSSAMVILGMAKL 307
 QY 302 DEAPQRVSKSKNAESTERESQDTVAENDDGFSSEWMAQRDLSHGHRSTPESRAA 361
 DB 308 DESSQAL--CLPYDE--NEEDSYDSFGE--PSIFVFPPLTGYRG----- 349
 QY 362 QELSSSTIAGDEDEBERGVKLGDFIFYSVLVGKASATASGDMNTTIACFVALIIGLCL 421
 DB 350 BEL-----EEBERGVKLGDFIFYSVLVGKAAAGSGDMNTTIACFVALIIGLCL 402
 QY 422 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 467
 DB 403 TLLLAIFKALPALPISITGIVFYPATDYLVOPFMDQAFHOFYI 448

Search completed: April 8, 2004, 17:03:53
 Job time : 49 secs